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<b>(21) International Application Number:</b> PCT/US99/19351 <b>(22) International Filing Date:</b> 24 August 1999 (24.08.99)  <b>(30) Priority Data:</b> <table border="0"><tr><td>60/097,638</td><td>24 August 1998 (24.08.98)</td><td>US</td></tr><tr><td>60/097,659</td><td>24 August 1998 (24.08.98)</td><td>US</td></tr><tr><td>60/099,618</td><td>9 September 1998 (09.09.98)</td><td>US</td></tr><tr><td>60/102,092</td><td>28 September 1998 (28.09.98)</td><td>US</td></tr><tr><td>60/109,978</td><td>25 November 1998 (25.11.98)</td><td>US</td></tr><tr><td>60/113,645</td><td>23 December 1998 (23.12.98)</td><td>US</td></tr><tr><td>60/113,646</td><td>23 December 1998 (23.12.98)</td><td>US</td></tr><tr><td>09/379,246</td><td>23 August 1999 (23.08.99)</td><td>US</td></tr></table> <b>(71) Applicant:</b> ALPHAGENE, INC. [US/US]; 260 West Cummings Park, Woburn, MA 01801 (US).  <b>(72) Inventors:</b> VALENZUELA, Dario; 260 West Cummings Park, Woburn, MA 01801 (US). YUAN, Olive; 260 West Cummings Park, Woburn, MA 01801 (US). HOFFMAN, Heidi; 260 West Cummings Park, Woburn, MA 01801 (US). HALL, Jeff; 260 West Cummings Park, Woburn, MA 01801 (US). RAPIEJKO, Peter; 260 West Cummings Park, Woburn, MA 01801 (US).	60/097,638	24 August 1998 (24.08.98)	US	60/097,659	24 August 1998 (24.08.98)	US	60/099,618	9 September 1998 (09.09.98)	US	60/102,092	28 September 1998 (28.09.98)	US	60/109,978	25 November 1998 (25.11.98)	US	60/113,645	23 December 1998 (23.12.98)	US	60/113,646	23 December 1998 (23.12.98)	US	09/379,246	23 August 1999 (23.08.99)	US	<b>(74) Agent:</b> SPRUNGER, Suzanne, A.; American Home Products Corporation, Patent & Trademark Dept. - 2B, One Campus Drive, Parsippany, NJ 07054 (US).  <b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
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<b>(54) Title:</b> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  <b>(57) Abstract</b>  Novel polynucleotides and the proteins encoded thereby are disclosed.																									

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## SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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This application is a continuation-in-part of the following applications:

- (1) provisional application Ser. No. 60/097,638 (GI 6908), filed August 24, 1998;
  - (2) provisional application Ser. No. 60/097,659 (GI 6909), filed August 24, 1998;
  - (3) provisional application Ser. No. 60/099,618 (GI 6910), filed September 9, 1998;
  - 10 (4) provisional application Ser. No. 60/102,092 (GI 6912), filed September 28, 1998;
  - (5) provisional application Ser. No. 60/109,978 (GI 6914), filed November 25, 1998;
  - (6) provisional application Ser. No. 60/113,645 (GI 6916), filed December 23, 1998; and
  - (7) provisional application Ser. No. 60/113,646 (GI 6917), filed December 23, 1998;
- all of which are incorporated by reference herein.

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

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BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques  
25 clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader  
30 sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the  
35 polynucleotides encoding them that the present invention is directed.

### SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 683 to nucleotide 934;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb11\_1 deposited with the ATCC under  
10 accession number 98846;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;
- (e) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone vb11\_1 deposited with the ATCC under accession number 98846;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;
- (g) a polynucleotide encoding a protein comprising the amino acid  
20 sequence of SEQ ID NO:2;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of  
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 683 to nucleotide 934; the nucleotide sequence of the full-length

protein coding sequence of clone vb11\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vb11\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
- (bb) the nucleotide sequence of the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 683 to nucleotide 934, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 683 to nucleotide 934, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 683 to nucleotide 934.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
- (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ

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ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 63 to nucleotide 482;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:3 from nucleotide 201 to nucleotide 482;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb12\_1 deposited with the ATCC under accession number 98846;
- (e) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb12\_1 deposited with the ATCC under accession number 98846;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the  
25 amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein  
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 63 to nucleotide 482; the nucleotide sequence of SEQ ID NO:3 from nucleotide 201 to nucleotide 482; the nucleotide sequence of the full-length protein coding sequence of clone vb12\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vb12\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 63 to nucleotide 482, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 63 to nucleotide 482, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 63 to nucleotide 482. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 201 to nucleotide 482, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 201 to nucleotide 482, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 201 to nucleotide 482.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

- (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 1195 to nucleotide 1527;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:5 from nucleotide 1468 to nucleotide 1527;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb14\_1 deposited with the ATCC under accession number 98846;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;



(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 1195 to nucleotide 1527; the nucleotide sequence of SEQ ID NO:5 from nucleotide 1468 to nucleotide 1527; the nucleotide sequence of the full-length protein coding sequence of clone vb14\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vb14\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846.

20 In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and
- (ab) the nucleotide sequence of the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 vb14\_1 deposited with the ATCC under accession number 98846;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated
- 30 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 1195 to nucleotide 1527, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 1195 to nucleotide 1527, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 1195 to

nucleotide 1527. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 1468 to nucleotide 1527, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from  
5 nucleotide 1468 to nucleotide 1527, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 1468 to nucleotide 1527.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:6;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 50 to amino acid 59 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 82 to nucleotide 294;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:7 from nucleotide 109 to nucleotide 294;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ve11\_1 deposited with the ATCC under accession number 98846;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ve11\_1 deposited with the ATCC under accession number 98846;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 82 to nucleotide 294; the nucleotide sequence of SEQ ID NO:7 from  
25 nucleotide 109 to nucleotide 294; the nucleotide sequence of the full-length protein coding sequence of clone ve11\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone ve11\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
30 of clone ve11\_1 deposited with the ATCC under accession number 98846. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
    - (ab) the nucleotide sequence of the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
    - (bb) the nucleotide sequence of the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending

contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 82 to nucleotide 294, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 82 to nucleotide 294, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 82 to nucleotide 294. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 109 to nucleotide 294, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 109 to nucleotide 294, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 109 to nucleotide 294.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 22 to nucleotide 468;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 118 to nucleotide 468;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number
- 10 98846;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 15 insert of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment
- 20 comprising eight contiguous amino acids of SEQ ID NO:10;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 22 to nucleotide 468; the nucleotide sequence of SEQ ID NO:9 from nucleotide 118 to nucleotide 468; the nucleotide sequence of the full-length protein coding sequence of clone vf2\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vf2\_1 deposited with

the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and



- (bb) the nucleotide sequence of the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 22 to nucleotide 468, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 22 to nucleotide 468, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 22 to nucleotide 468. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 118 to nucleotide 468, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 118 to nucleotide 468, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 118 to nucleotide 468.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:10.

5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- 10       (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 124 to nucleotide 1641;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 262 to nucleotide 1641;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vg2\_1 deposited with the ATCC under  
15       accession number 98846;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature  
20       protein coding sequence of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (h)     a polynucleotide encoding a protein comprising the amino acid  
25       sequence of SEQ ID NO:12;
- (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of  
30       (a)-(g) above;
- (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 124 to nucleotide 1641; the nucleotide sequence of SEQ ID NO:11 from nucleotide 262 to nucleotide 1641; the nucleotide sequence of the full-length protein coding sequence of clone vg2\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vg2\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 248 to amino acid 257 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 124 to nucleotide 1641, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 124 to nucleotide 1641, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 124 to nucleotide 1641. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 262 to nucleotide 1641, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 262 to nucleotide 1641, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 262 to nucleotide 1641.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and

(c) the amino acid sequence encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 248 to amino acid 257 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 380 to nucleotide 892;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 416 to nucleotide 892;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vj1\_1 deposited with the ATCC under accession number 98846;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vj1\_1 deposited with the ATCC under accession number 98846;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 380 to nucleotide 892; the nucleotide sequence of SEQ ID NO:13  
15 from nucleotide 416 to nucleotide 892; the nucleotide sequence of the full-length protein coding sequence of clone vj1\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vj1\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
20 of clone vj1\_1 deposited with the ATCC under accession number 98846. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide  
25 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:13; and

5 (ab) the nucleotide sequence of the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and  
25 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 380 to nucleotide 892, and extending contiguously from a nucleotide sequence  
30 corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 380 to nucleotide 892, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 380 to nucleotide 892. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 416 to nucleotide 892, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 416 to nucleotide 892, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 416 to nucleotide 892.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the  
10 fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred  
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence  
20 from amino acid 80 to amino acid 89 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
25 NO:15 from nucleotide 62 to nucleotide 1057;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 659 to nucleotide 1057;
- (d) a polynucleotide comprising the nucleotide sequence of the full-  
30 length protein coding sequence of clone v11\_1 deposited with the ATCC under accession number 98846;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone v11\_1 deposited with the ATCC under accession number 98846;



- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vl1\_1 deposited with the ATCC under accession number 98846;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 62 to nucleotide 1057; the nucleotide sequence of SEQ ID NO:15 from nucleotide 659 to nucleotide 1057; the nucleotide sequence of the full-length protein coding sequence of clone vl1\_1 deposited with the ATCC under accession number 98846; or the nucleotide sequence of a mature protein coding sequence of clone vl1\_1 deposited with the ATCC under accession number 98846. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 161 to amino acid 170 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5           (a)    a process comprising the steps of:
- (i)    preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:15, but excluding the poly(A) tail at the
- 10               3' end of SEQ ID NO:15; and
- (ab)   the nucleotide sequence of the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846;
- (ii)   hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15              (iii)   isolating the DNA polynucleotides detected with the probe(s);

and

- (b)    a process comprising the steps of:
- (i)    preparing one or more polynucleotide primers that
- 20               hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba)   SEQ ID NO:15, but excluding the poly(A) tail at the
- 3' end of SEQ ID NO:15; and
- (bb)   the nucleotide sequence of the cDNA insert of clone
- 25               vl1\_1 deposited with the ATCC under accession number 98846;
- (ii)   hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- (iv)   isolating the polynucleotide products of step (b)(iii).

- 30   Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 62 to nucleotide 1057, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 62 to nucleotide 1057, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 62 to nucleotide 1057. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 659 to nucleotide 1057, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 659 to nucleotide 1057, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 659 to nucleotide 1057.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 161 to amino acid 170 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 74 to nucleotide 529;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 140 to nucleotide 529;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vk2\_1 deposited with the ATCC under accession number 98838;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vk2\_1 deposited with the ATCC under accession number 98838;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 74 to nucleotide 529; the nucleotide sequence of SEQ ID NO:17 from nucleotide 140 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone vk2\_1 deposited with the ATCC under accession number 98838; or the nucleotide sequence of a mature protein coding sequence of clone vk2\_1 deposited with the ATCC under accession number 98838. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

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of clone vk2\_1 deposited with the ATCC under accession number 98838. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, 5 most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 71 to amino acid 80 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 10 ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize 15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
    - (ab) the nucleotide sequence of the cDNA insert of clone 20 vk2\_1 deposited with the ATCC under accession number 98838;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 30 (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 74 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 74 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide
- 15 74 to nucleotide 529. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 140 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 140 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:17 from nucleotide 140 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;

- the protein being substantially free from other mammalian proteins. Preferably such
- 30 protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 71 to amino acid 80 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5           (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 174 to nucleotide 3170;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10       NO:19 from nucleotide 1098 to nucleotide 3170;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (e)     a polynucleotide encoding the full-length protein encoded by the  
15       cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb21\_1 deposited with the ATCC under accession number 98862;
- 20       (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i)     a polynucleotide encoding a protein comprising a fragment of the  
25       amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k)     a polynucleotide which encodes a species homologue of the protein  
30       of (h) or (i) above ;
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 174 to nucleotide 3170; the nucleotide sequence of SEQ ID NO:19 from nucleotide 1098 to nucleotide 3170; the nucleotide sequence of the full-length protein coding sequence of clone vb21\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vb21\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 494 to amino acid 503 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);



and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 174 to nucleotide 3170, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 174 to nucleotide 3170, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 174 to nucleotide 3170. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 1098 to nucleotide 3170, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 1098 to nucleotide 3170, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 1098 to nucleotide 3170.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 494 to amino acid 503 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 74 to nucleotide 1453;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 224 to nucleotide 1453;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc35\_1 deposited with the ATCC under accession number 98862;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc35\_1 deposited with the ATCC under accession number 98862;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 74 to nucleotide 1453; the nucleotide sequence of SEQ ID NO:21 from nucleotide 224 to nucleotide 1453; the nucleotide sequence of the full-length protein coding sequence of clone vc35\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc35\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 225 to amino acid 234 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(ab) the nucleotide sequence of the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 74 to nucleotide 1453, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 74 to nucleotide 1453, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide

74 to nucleotide 1453. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 224 to nucleotide 1453, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 224 to nucleotide 1453, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 224 to nucleotide 1453.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:22;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 225 to amino acid 234 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 135 to nucleotide 368;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:23 from nucleotide 243 to nucleotide 368;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc36\_1 deposited with the ATCC under accession number 98862;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;

5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc36\_1 deposited with the ATCC under accession number 98862;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;

10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 135 to nucleotide 368; the nucleotide sequence of SEQ ID NO:23 from nucleotide 243 to nucleotide 368; the nucleotide sequence of the full-length protein coding sequence of clone vc36\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc36\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
5 ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
15 vc36\_1 deposited with the ATCC under accession number 98862;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;
    - (ii) hybridizing said primer(s) to human genomic DNA in  
30 conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 135 to nucleotide 368, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 135 to nucleotide 368, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 135 to nucleotide 368. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 243 to nucleotide 368, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 243 to nucleotide 368, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 243 to nucleotide 368.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 34 to amino acid 43 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;



- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 370 to nucleotide 1662;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc38\_1 deposited with the ATCC under accession number 98862;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc38\_1 deposited with the ATCC under accession number 98862;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc38\_1 deposited with the ATCC under accession number 98862;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc38\_1 deposited with the ATCC under accession number 98862;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- 15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 370 to nucleotide 1662; the nucleotide sequence of the full-length protein coding sequence of clone vc38\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc38\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc38\_1 deposited with the ATCC under accession number 98862.

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In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a  
5 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize  
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:25, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:25; and

- (ab) the nucleotide sequence of the cDNA insert of clone  
vc38\_1 deposited with the ATCC under accession number 98862;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the  
probe(s);

and

25 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:25, but excluding the poly(A) tail at the  
30 3' end of SEQ ID NO:25; and

- (bb) the nucleotide sequence of the cDNA insert of clone  
vc38\_1 deposited with the ATCC under accession number 98862;

- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide  
10 1662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 370 to nucleotide 1662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 370 to nucleotide 1662.

In other embodiments, the present invention provides a composition comprising  
15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
- (b) a fragment of the amino acid sequence of SEQ ID NO:26, the  
fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone vc38\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:26.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 105 to nucleotide 365;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 147 to nucleotide 365;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc39\_1 deposited with the ATCC under accession number 98862;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc39\_1 deposited with the ATCC under accession number 98862;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 105 to nucleotide 365; the nucleotide sequence of SEQ ID NO:27 from nucleotide 147 to nucleotide 365; the nucleotide sequence of the full-length protein coding sequence of clone vc39\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc39\_1 deposited

with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

- (bb) the nucleotide sequence of the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 105 to nucleotide 365, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 105 to nucleotide 365, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 105 to nucleotide 365. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 147 to nucleotide 365, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 147 to nucleotide 365, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 147 to nucleotide 365.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:28.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 35 to nucleotide 1066;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 128 to nucleotide 1066;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc40\_1 deposited with the ATCC under  
15 accession number 98862;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc40\_1 deposited with the ATCC under accession number 98862;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:30;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 35 to nucleotide 1066; the nucleotide sequence of SEQ ID NO:29 from nucleotide 128 to nucleotide 1066; the nucleotide sequence of the full-length protein coding sequence of clone vc40\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc40\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 167 to amino acid 176 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);



and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(bb) the nucleotide sequence of the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 35 to nucleotide 1066, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 35 to nucleotide 1066, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 35 to nucleotide 1066. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 128 to nucleotide 1066, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 128 to nucleotide 1066, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 128 to nucleotide 1066.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 167 to amino acid 176 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 553;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:31 from nucleotide 104 to nucleotide 553;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc46\_1 deposited with the ATCC under accession number 98862;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 553; the nucleotide sequence of SEQ ID NO:31 from nucleotide 104 to nucleotide 553; the nucleotide sequence of the full-length protein coding sequence of clone vc46\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc46\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 81 to amino acid 90 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and
- (ab) the nucleotide sequence of the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 vc46\_1 deposited with the ATCC under accession number 98862;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 553, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 553, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide

38 to nucleotide 553. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 104 to nucleotide 553, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from  
5 nucleotide 104 to nucleotide 553, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 104 to nucleotide 553.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:32;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 81 to amino acid 90 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 164 to nucleotide 2548;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:33 from nucleotide 242 to nucleotide 2548;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc49\_1 deposited with the ATCC under accession number 98862;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc49\_1 deposited with the ATCC under accession number 98862;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 164 to nucleotide 2548; the nucleotide sequence of SEQ ID NO:33 from nucleotide 242 to nucleotide 2548; the nucleotide sequence of the full-length protein coding sequence of clone vc49\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc49\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 392 to amino acid 401 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
5 ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
15 vc49\_1 deposited with the ATCC under accession number 98862;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);  
20 and
  - (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
25
      - (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
      - (bb) the nucleotide sequence of the cDNA insert of clone  
vc49\_1 deposited with the ATCC under accession number 98862;
      - (ii) hybridizing said primer(s) to human genomic DNA in  
30 conditions at least as stringent as 4X SSC at 50 degrees C;
      - (iii) amplifying human DNA sequences; and
      - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 164 to nucleotide 2548, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 164 to nucleotide 2548, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 164 to nucleotide 2548. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 242 to nucleotide 2548, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 242 to nucleotide 2548, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 242 to nucleotide 2548.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 392 to amino acid 401 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;



- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 150 to nucleotide 776;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 246 to nucleotide 776;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 150 to nucleotide 776; the nucleotide sequence of SEQ ID NO:35 from nucleotide 246 to nucleotide 776; the nucleotide sequence of the full-length protein coding sequence of clone vc50\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc50\_1 deposited

with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

- (bb) the nucleotide sequence of the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 150 to nucleotide 776, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 150 to nucleotide 776, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 150 to nucleotide 776. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 246 to nucleotide 776, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 246 to nucleotide 776, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 246 to nucleotide 776.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:36.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:37 from nucleotide 139 to nucleotide 1308;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 211 to nucleotide 1308;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc51\_1 deposited with the ATCC under  
15 accession number 98862;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
20 protein coding sequence of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:38;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 139 to nucleotide 1308; the nucleotide sequence of SEQ ID NO:37 from nucleotide 211 to nucleotide 1308; the nucleotide sequence of the full-length protein coding sequence of clone vc51\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc51\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 190 to amino acid 199 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 139 to nucleotide 1308, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 139 to nucleotide 1308, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 139 to nucleotide 1308. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 211 to nucleotide 1308, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 211 to nucleotide 1308, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 211 to nucleotide 1308.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 190 to amino acid 199 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 21 to nucleotide 1142;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 114 to nucleotide 1142;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc52\_1 deposited with the ATCC under accession number 98862;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc52\_1 deposited with the ATCC under accession number 98862;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 21 to nucleotide 1142; the nucleotide sequence of SEQ ID NO:39  
15 from nucleotide 114 to nucleotide 1142; the nucleotide sequence of the full-length protein coding sequence of clone vc52\_1 deposited with the ATCC under accession number 98862; or the nucleotide sequence of a mature protein coding sequence of clone vc52\_1 deposited with the ATCC under accession number 98862. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
20 of clone vc52\_1 deposited with the ATCC under accession number 98862. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide  
25 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 182 to amino acid 191 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
- (ab) the nucleotide sequence of the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 vc52\_1 deposited with the ATCC under accession number 98862;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 21 to nucleotide 1142, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 21 to nucleotide 1142, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide

21 to nucleotide 1142. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 114 to nucleotide 1142, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from  
5 nucleotide 114 to nucleotide 1142, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 114 to nucleotide 1142.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:40;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 182 to amino acid 191 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 13 to nucleotide 1416;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:41 from nucleotide 346 to nucleotide 1416;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc33\_1 deposited with the ATCC under accession number 98886;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc33\_1 deposited with the ATCC under accession number 98886;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 13 to nucleotide 1416; the nucleotide sequence of SEQ ID NO:41 from nucleotide 346 to nucleotide 1416; the nucleotide sequence of the full-length protein coding sequence of clone vc33\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vc33\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 229 to amino acid 238 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
      - (ab) the nucleotide sequence of the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
      - (bb) the nucleotide sequence of the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 13 to nucleotide 1416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 13 to nucleotide 1416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 13 to nucleotide 1416. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 346 to nucleotide 1416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 346 to nucleotide 1416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 346 to nucleotide 1416.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 229 to amino acid 238 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 232 to nucleotide 1461;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 280 to nucleotide 1461;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc34\_1 deposited with the ATCC under accession number 98886;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc34\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:43.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 232 to nucleotide 1461; the nucleotide sequence of SEQ ID NO:43 from nucleotide 280 to nucleotide 1461; the nucleotide sequence of the full-length protein coding sequence of clone vc34\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vc34\_1 deposited

with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 200 to amino acid 209 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

- (bb) the nucleotide sequence of the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 232 to nucleotide 1461, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:43 from nucleotide 232 to nucleotide 1461, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 232 to nucleotide 1461. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 280 to nucleotide 1461, and extending contiguously from a  
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 280 to nucleotide 1461, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 280 to nucleotide 1461.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
- (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
30 vc34\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably



comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 200 to amino acid 209 of SEQ ID NO:44.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:45 from nucleotide 1922 to nucleotide 2350;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 2237 to nucleotide 2350;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc47\_1 deposited with the ATCC under  
15 accession number 98886;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
20 protein coding sequence of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:46;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 1922 to nucleotide 2350; the nucleotide sequence of SEQ ID NO:45 from nucleotide 2237 to nucleotide 2350; the nucleotide sequence of the full-length protein coding sequence of clone vc47\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vc47\_1 deposited with the ATCC under accession number 98886. In other preferred  
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15  
embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably  
20  
25  
30  
thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize  
25  
30  
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 1922 to nucleotide 2350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 1922 to nucleotide 2350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 1922 to nucleotide 2350. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 2237 to nucleotide 2350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 2237 to nucleotide 2350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 2237 to nucleotide 2350.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:46;

(b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 66 to amino acid 75 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 111 to nucleotide 1337;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 246 to nucleotide 1337;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc54\_1 deposited with the ATCC under accession number 98886;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc54\_1 deposited with the ATCC under accession number 98886;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 111 to nucleotide 1337; the nucleotide sequence of SEQ ID NO:47  
15 from nucleotide 246 to nucleotide 1337; the nucleotide sequence of the full-length protein coding sequence of clone vc54\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vc54\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
20 of clone vc54\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide  
25 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 199 to amino acid 208 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and
  - (ab) the nucleotide sequence of the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 111 to nucleotide 1337, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 111 to nucleotide 1337, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide

111 to nucleotide 1337. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 246 to nucleotide 1337, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from  
5 nucleotide 246 to nucleotide 1337, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 246 to nucleotide 1337.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:48;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 199 to amino acid 208 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 189 to nucleotide 1637;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:49 from nucleotide 270 to nucleotide 1637;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc57\_1 deposited with the ATCC under accession number 98886;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc57\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 189 to nucleotide 1637; the nucleotide sequence of SEQ ID NO:49  
25 from nucleotide 270 to nucleotide 1637; the nucleotide sequence of the full-length protein coding sequence of clone vc57\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vc57\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
30 of clone vc57\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide



encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 236 to amino acid 245 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 189 to nucleotide 1637, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 189 to nucleotide 1637, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 189 to nucleotide 1637. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 270 to nucleotide 1637, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 270 to nucleotide 1637, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 270 to nucleotide 1637.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 236 to amino acid 245 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 15 to nucleotide 1934;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 1704 to nucleotide 1934;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 15 to nucleotide 1934; the nucleotide sequence of SEQ ID NO:51 from nucleotide 1704 to nucleotide 1934; the nucleotide sequence of the full-length protein coding sequence of clone ve13\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone

ve13\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886.

In further preferred embodiments, the present invention provides a polynucleotide  
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of  
10 SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 315 to amino acid 324 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:51, but excluding the poly(A) tail at the  
20 3' end of SEQ ID NO:51; and
- (ab) the nucleotide sequence of the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that  
30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

- (bb) the nucleotide sequence of the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

10 ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 15 to nucleotide 1934, and extending contiguously from a nucleotide sequence corresponding to the 5' end

15 of said sequence of SEQ ID NO:51 from nucleotide 15 to nucleotide 1934, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 15 to nucleotide 1934. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 1704 to nucleotide 1934, and extending contiguously from a

20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 1704 to nucleotide 1934, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 1704 to nucleotide 1934.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 ve13\_1 deposited with the ATCC under accession number 98886;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 315 to amino acid 324 of SEQ ID NO:52.

5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:53 from nucleotide 240 to nucleotide 503;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 318 to nucleotide 503;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ve16\_1 deposited with the ATCC under  
15 accession number 98886;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
20 protein coding sequence of clone ve16\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 240 to nucleotide 503; the nucleotide sequence of SEQ ID NO:53 from nucleotide 318 to nucleotide 503; the nucleotide sequence of the full-length protein coding sequence of clone ve16\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone ve16\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and
    - (ab) the nucleotide sequence of the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 240 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 240 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 240 to nucleotide 503. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 318 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 318 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 318 to nucleotide 503.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;



(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 11 to nucleotide 1063;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1063;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vf3\_1 deposited with the ATCC under accession number 98886;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vf3\_1 deposited with the ATCC under accession number 98886;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 11 to nucleotide 1063; the nucleotide sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1063; the nucleotide sequence of the full-length protein coding sequence of clone vf3\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vf3\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
  - (ab) the nucleotide sequence of the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 11 to nucleotide 1063, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 11 to nucleotide 1063, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide

11 to nucleotide 1063. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1063, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from  
5 nucleotide 71 to nucleotide 1063, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1063.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:56;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 542 to nucleotide 886;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:57 from nucleotide 755 to nucleotide 886;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vj2\_1 deposited with the ATCC under accession number 98886;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vj2\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 542 to nucleotide 886; the nucleotide sequence of SEQ ID NO:57 from nucleotide 755 to nucleotide 886; the nucleotide sequence of the full-length protein coding sequence of clone vj2\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vj2\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 542 to nucleotide 886, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 542 to nucleotide 886, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 542 to nucleotide 886. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 755 to nucleotide 886, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 755 to nucleotide 886, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 755 to nucleotide 886.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 52 to amino acid 61 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 30 to nucleotide 344;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 84 to nucleotide 344;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 30 to nucleotide 344; the nucleotide sequence of SEQ ID NO:59 from nucleotide 84 to nucleotide 344; the nucleotide sequence of the full-length protein coding sequence of clone vp7\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vp7\_1 deposited



with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that
  - 30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

- (bb) the nucleotide sequence of the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 30 to nucleotide 344, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 30 to nucleotide 344, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 30 to nucleotide 344. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 84 to nucleotide 344, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 84 to nucleotide 344, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 84 to nucleotide 344.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:60.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:61 from nucleotide 23 to nucleotide 757;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 757;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp8\_1 deposited with the ATCC under  
15 accession number 98886;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
20 protein coding sequence of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:62;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 23 to nucleotide 757; the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 757; the nucleotide sequence of the full-length protein coding sequence of clone vp8\_1 deposited with the ATCC under accession number 98886; or the nucleotide sequence of a mature protein coding sequence of clone vp8\_1 deposited with the ATCC under accession number 98886. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 23 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 23 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 23 to nucleotide 757. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 757.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 1048 to nucleotide 3726;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb22\_1 deposited with the ATCC under
- 20 accession number 98933;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb22\_1 deposited with the ATCC under accession number 98933;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:63.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 1048 to nucleotide 3726; the nucleotide sequence of the full-length protein coding sequence of clone vb22\_1 deposited with the ATCC under accession number 98933; or the nucleotide sequence of a mature protein coding sequence of clone vb22\_1 deposited with the ATCC under accession number 98933. In other preferred  
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably  
20 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 441 to amino acid 450 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

- (ab) the nucleotide sequence of the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vb22\_1 deposited with the ATCC under accession number 98933;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 1048 to nucleotide 3726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 1048 to nucleotide 3726, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide
- 30 1048 to nucleotide 3726.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;



(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933;

- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 441 to amino acid 450 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 134 to nucleotide 667;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:65 from nucleotide 191 to nucleotide 667;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc48\_1 deposited with the ATCC under accession number 98933;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 134 to nucleotide 667; the nucleotide sequence of SEQ ID NO:65 from nucleotide 191 to nucleotide 667; the nucleotide sequence of the full-length protein coding sequence of clone vc48\_1 deposited with the ATCC under accession number 98933; or the nucleotide sequence of a mature protein coding sequence of clone vc48\_1 deposited with the ATCC under accession number 98933. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and
- (ab) the nucleotide sequence of the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 15 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 20 vc48\_1 deposited with the ATCC under accession number 98933;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 134 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 134 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide

134 to nucleotide 667. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 191 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 191 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 191 to nucleotide 667.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:66;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 65 to nucleotide 457;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:67 from nucleotide 158 to nucleotide 457;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp3\_1 deposited with the ATCC under accession number 98933;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp3\_1 deposited with the ATCC under accession number 98933;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 65 to nucleotide 457; the nucleotide sequence of SEQ ID NO:67  
25 from nucleotide 158 to nucleotide 457; the nucleotide sequence of the full-length protein coding sequence of clone vp3\_1 deposited with the ATCC under accession number 98933; or the nucleotide sequence of a mature protein coding sequence of clone vp3\_1 deposited with the ATCC under accession number 98933. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
30 of clone vp3\_1 deposited with the ATCC under accession number 98933. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (bb) the nucleotide sequence of the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 65 to nucleotide 457, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 65 to nucleotide 457, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 65 to nucleotide 457. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 158 to nucleotide 457, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 158 to nucleotide 457, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 158 to nucleotide 457.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
- (b) a fragment of the amino acid sequence of SEQ ID NO:68, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 60 to amino acid 69 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 29 to nucleotide 1387;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 113 to nucleotide 1387;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number  
10 207012;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
15 insert of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment  
20 comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 29 to nucleotide 1387; the nucleotide sequence of SEQ ID NO:69 from nucleotide 113 to nucleotide 1387; the nucleotide sequence of the full-length protein coding sequence of clone vc61\_1 deposited with the ATCC under accession number 207012; or the nucleotide sequence of a mature protein coding sequence of clone vc61\_1



deposited with the ATCC under accession number 207012. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number 207012. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 221 to amino acid 230 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number 207012;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

- (bb) the nucleotide sequence of the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 29 to nucleotide 1387, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:69 from nucleotide 29 to nucleotide 1387, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 29 to nucleotide 1387. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 113 to nucleotide 1387, and extending contiguously from a  
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 113 to nucleotide 1387, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 113 to nucleotide 1387.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
30 vc61\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 221 to amino acid 230 of SEQ ID NO:70.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:71 from nucleotide 44 to nucleotide 1513;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 92 to nucleotide 1513;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 1 to nucleotide 458;
- 15 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp15\_1 deposited with the ATCC under accession number 207012;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number  
20 207012;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp15\_1 deposited with the ATCC under accession number 207012;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA  
25 insert of clone vp15\_1 deposited with the ATCC under accession number 207012;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment  
30 comprising eight contiguous amino acids of SEQ ID NO:72;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 44 to nucleotide 1513; the nucleotide sequence of SEQ ID NO:71 from nucleotide 92 to nucleotide 1513; the nucleotide sequence of SEQ ID NO:71 from nucleotide 1 to nucleotide 458; the nucleotide sequence of the full-length protein coding sequence of clone vp15\_1 deposited with the ATCC under accession number 207012; or the nucleotide sequence of a mature protein coding sequence of clone vp15\_1 deposited with the ATCC under accession number 207012. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number 207012. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72 from amino acid 1 to amino acid 139. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

- (ab) the nucleotide sequence of the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number 207012;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vp15\_1 deposited with the ATCC under accession number 207012;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 44 to nucleotide 1513, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 44 to nucleotide 1513, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide
- 30 44 to nucleotide 1513. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 92 to nucleotide 1513, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 92 to nucleotide 1513, to a nucleotide sequence corresponding to the 3' end of

said sequence of SEQ ID NO:71 from nucleotide 92 to nucleotide 1513. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 1 to nucleotide 458, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 1 to nucleotide 458, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 1 to nucleotide 458.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) the amino acid sequence of SEQ ID NO:72 from amino acid 1 to amino acid 139;
- (c) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (d) the amino acid sequence encoded by the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72 or the amino acid sequence of SEQ ID NO:72 from amino acid 1 to amino acid 139. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 348 to nucleotide 743;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 414 to nucleotide 743;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp17\_1 deposited with the ATCC under accession number 207012;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp17\_1 deposited with the ATCC under accession number 207012;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 25 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 348 to nucleotide 743; the nucleotide sequence of SEQ ID NO:73 from nucleotide 414 to nucleotide 743; the nucleotide sequence of the full-length protein coding sequence of clone vp17\_1 deposited with the ATCC under accession number

30 207012; or the nucleotide sequence of a mature protein coding sequence of clone vp17\_1 deposited with the ATCC under accession number 207012. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012. In further preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

- (ab) the nucleotide sequence of the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

- (bb) the nucleotide sequence of the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and



(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 348 to nucleotide 743, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 348 to nucleotide 743, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 348 to nucleotide 743. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 414 to nucleotide 743, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 414 to nucleotide 743, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 414 to nucleotide 743.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 144 to nucleotide 461;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp19\_1 deposited with the ATCC under accession number 207012;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp19\_1 deposited with the ATCC under accession number 207012;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp19\_1 deposited with the ATCC under  
15 accession number 207012;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp19\_1 deposited with the ATCC under accession number 207012;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 144 to nucleotide 461; the nucleotide sequence of the full-length protein coding sequence of clone vp19\_1 deposited with the ATCC under accession

number 207012; or the nucleotide sequence of a mature protein coding sequence of clone vp19\_1 deposited with the ATCC under accession number 207012. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp19\_1 deposited with the ATCC under accession number  
5 207012. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or  
10 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
20 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and  
(ab) the nucleotide sequence of the cDNA insert of clone vp19\_1 deposited with the ATCC under accession number 207012;  
(ii) hybridizing said probe(s) to human genomic DNA in  
25 conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:  
30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
  - (ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

- (bb) the nucleotide sequence of the cDNA insert of clone  
vp19\_1 deposited with the ATCC under accession number 207012;
- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but  
excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 144 to nucleotide  
461, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:75 from nucleotide 144 to nucleotide 461, to a nucleotide  
sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide  
144 to nucleotide 461.

In other embodiments, the present invention provides a composition comprising  
a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
- (b) a fragment of the amino acid sequence of SEQ ID NO:76, the  
fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
25 vp19\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins. Preferably such  
protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred  
embodiments, the present invention provides a protein comprising a fragment of the  
amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:76 having biological activity, the fragment comprising the amino acid sequence  
from amino acid 48 to amino acid 57 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 54 to nucleotide 368;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 141 to nucleotide 368;
- 10 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 51 to nucleotide 332;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq1\_1 deposited with the ATCC under accession number 207012;
- 15 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq1\_1 deposited with the ATCC under accession number 207012;
- 20 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- 25 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 54 to nucleotide 368; the nucleotide sequence of SEQ ID NO:77 from nucleotide 141 to nucleotide 368; the nucleotide sequence of SEQ ID NO:77 from nucleotide 51 to nucleotide 332; the nucleotide sequence of the full-length protein coding sequence of clone vq1\_1 deposited with the ATCC under accession number 207012; or the nucleotide sequence of a mature protein coding sequence of clone vq1\_1 deposited with the ATCC under accession number 207012. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
    - (ab) the nucleotide sequence of the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 54 to nucleotide  
25 368, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 54 to nucleotide 368, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 54 to nucleotide 368. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
30 NO:77 from nucleotide 141 to nucleotide 368, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 141 to nucleotide 368, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 141 to nucleotide 368. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide

sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 51 to nucleotide 332, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 51 to nucleotide 332, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from  
5 nucleotide 51 to nucleotide 332.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- 10 (b) the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 93;
- (c) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (d) the amino acid sequence encoded by the cDNA insert of clone  
15 vq1\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78 or the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid  
20 sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:78.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:79 from nucleotide 2 to nucleotide 1018;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 53 to nucleotide 1018;



- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp14\_1 deposited with the ATCC under accession number 207011;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp14\_1 deposited with the ATCC under accession number 207011;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 25 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 2 to nucleotide 1018; the nucleotide sequence of SEQ ID NO:79 from nucleotide 53 to nucleotide 1018; the nucleotide sequence of the full-length protein coding sequence of clone vp14\_1 deposited with the ATCC under accession number

30 207011; or the nucleotide sequence of a mature protein coding sequence of clone vp14\_1 deposited with the ATCC under accession number 207011. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011. In further preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence  
5 of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 164 to amino acid 173 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

30 (bb) the nucleotide sequence of the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 2 to nucleotide 1018, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 2 to nucleotide 1018, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 2 to nucleotide 1018. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 53 to nucleotide 1018, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 53 to nucleotide 1018, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 53 to nucleotide 1018.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
- (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 164 to amino acid 173 of SEQ ID NO:80.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or  
5 modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- 10 (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which  
15 specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.  
20

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

#### 25 DETAILED DESCRIPTION

##### ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone  
30 in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have

determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

10        Clone "vb11\_1"

A polynucleotide of the present invention has been identified as clone "vb11\_1". vb11\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb11\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb11\_1 protein").

The nucleotide sequence of vb11\_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb11\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Another potential vb11\_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 84 to 236 of SEQ ID NO:1 is reported in SEQ ID NO:121. Amino acids 13 to 25 of SEQ ID NO:121 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26 of SEQ ID NO:121. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:121.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb11\_1 should be approximately 1751 bp.

The nucleotide sequence disclosed herein for vb11\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb11\_1 demonstrated at least some similarity with sequences identified as N94870 (yy63b05.r1 Homo sapiens cDNA clone 278193 5'). Based upon sequence similarity, vb11\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane

domain within the vb11\_1 protein sequence centered around amino acid 27 of SEQ ID NO:2.

Clone "vb12\_1"

5 A polynucleotide of the present invention has been identified as clone "vb12\_1". vb12\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb12\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb12\_1 protein").

10 The nucleotide sequence of vb12\_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb12\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 34 to 46 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted  
15 mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb12\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 vb12\_1 should be approximately 2289 bp.

The nucleotide sequence disclosed herein for vb12\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb12\_1 demonstrated at least some similarity with sequences identified as AA426009 (zw49e11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA  
25 clone 773420 3', mRNA sequence). Based upon sequence similarity, vb12\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the vb12\_1 protein sequence, centered around amino acids 11, 60, and 104 of SEQ ID NO:4, respectively. The nucleotide sequence of vb12\_1 indicates that it may contain a THE1B  
30 repeat sequence.

vb12\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 17 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "vb14\_1"

A polynucleotide of the present invention has been identified as clone "vb14\_1". vb14\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb14\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb14\_1 protein").

The nucleotide sequence of vb14\_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb14\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 79 to 91 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 92. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb14\_1 protein. Another potential vb14\_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 182 to 484 of SEQ ID NO:5 is reported in SEQ ID NO:122.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb14\_1 should be approximately 2377 bp.

The nucleotide sequence disclosed herein for vb14\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb14\_1 demonstrated at least some similarity with sequences identified as AF007149 (Homo sapiens clone 23568, 23621, 23795, 23873 and 23874 mRNA sequences), AF070612 (Homo sapiens clone 24771 mRNA sequence), T23635 (Human gene signature HUMGS05495; standard; cDNA to mRNA), and W02197 (za57e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 296670 5', mRNA sequence). Based upon sequence similarity, vb14\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "ve11\_1"

A polynucleotide of the present invention has been identified as clone "ve11\_1". ve11\_1 was isolated from a human adult brain (Alzheimer's hippocampus level 7) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis

of computer analysis of the amino acid sequence of the encoded protein. ve11\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ve11\_1 protein").

The nucleotide sequence of ve11\_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ve11\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 1 to 9 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 10. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ve11\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ve11\_1 should be approximately 984 bp.

The nucleotide sequence disclosed herein for ve11\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ve11\_1 demonstrated at least some similarity with sequences identified as F22745 (H.sapiens EST sequence (LL45/C09) from skeletal muscle, mRNA sequence) and Q60824 (Human brain Expressed Sequence Tag EST00928; standard; DNA). Based upon sequence similarity, ve11\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ve11\_1 protein sequence centered around amino acid 35 of SEQ ID NO:8.

#### Clone "vf2\_1"

A polynucleotide of the present invention has been identified as clone "vf2\_1". vf2\_1 was isolated from a human adult heart cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf2\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vf2\_1 protein").

The nucleotide sequence of vf2\_1 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vf2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 20 to 32



of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vf2\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vf2\_1 should be approximately 1162 bp.

The nucleotide sequence disclosed herein for vf2\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vf2\_1 demonstrated at least some similarity with sequences identified as AA605037 (no68h10.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA clone IMAGE:1112035 similar to contains Alu repetitive element;contains element THR repetitive element; mRNA sequence). Based upon sequence similarity, vf2\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vf2\_1 protein sequence, one centered around amino acid 30 and another around amino acid 70 of SEQ ID NO:10. The nucleotide sequence of vf2\_1 indicates that it may contain an Alu repetitive element.

Clone "vg2\_1"

A polynucleotide of the present invention has been identified as clone "vg2\_1". vg2\_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vg2\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vg2\_1 protein").

The nucleotide sequence of vg2\_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vg2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 34 to 46 of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the vg2\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vg2\_1 should be approximately 1993 bp.

- 5       The nucleotide sequence disclosed herein for vg2\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vg2\_1 demonstrated at least some similarity with sequences identified as AA830272 (oc45g11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE 1352708 3' similar to TR Q92853 Q92853 HU-K4; mRNA sequence) and D31740
- 10 (Homo sapiens DNA, CpG island). The predicted amino acid sequence disclosed herein for vg2\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vg2\_1 protein demonstrated at least some similarity to sequences identified as AF026124 (schwannoma-associated protein [Mus musculus]) and U60644 (HU-K4 [Homo sapiens]). Based upon sequence similarity,
- 15 vg2\_1 proteins and each similar protein or peptide may share at least some activity. Profile hidden markov model analysis (Eddy, S. R., 1996, *Curr. Opin. Struct. Biol.* 6(3): 361-365; incorporated by reference herein) of the predicted vg2\_1 protein revealed two phospholipase D active sites (amino acid residues 209 to 236 and 423 to 449 of SEQ ID NO:12). Phospholipase D (PLD) genes are members of a superfamily that is defined by
- 20 several highly conserved motifs. In mammals, it has been proposed that phospholipase D plays a role in membrane vesicular trafficking and in signal transduction. Using site-directed mutagenesis, twenty-five point mutants have been made in human PLD1 (hPLD1) and then characterized (Sung *et al.*, 1997, *EMBO J.* 16(15): 4519-4530; which is incorporated by reference herein). Sung *et al.* found that a motif (HxKxxxD; see for
- 25 example amino acids 214-221 of SEQ ID NO:12) and a serine/threonine conserved in all members of the PLD superfamily are critical for PLD biochemical activity, suggesting a possible catalytic mechanism. The vg2\_1 clone appears to encode a membrane protein that may be a phospholipase related to the phospholipase D family. The TopPredII computer program predicts four potential transmembrane domains within the vg2\_1
- 30 protein sequence, centered around amino acids 40, 305, 330, and 455 of SEQ ID NO:12, respectively.

Clone "vj1\_1"

A polynucleotide of the present invention has been identified as clone "vj1\_1". vj1\_1 was isolated from a human fetal brain cDNA library (enriched for G-protein-coupled receptors) and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vj1\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vj1\_1 protein").

The nucleotide sequence of vj1\_1 as presently determined is reported in SEQ ID NO:13. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vj1\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 1 to 12 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 13. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vj1\_1 protein. Another potential vj1\_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 1795 to 2064 of SEQ ID NO:13 is reported in SEQ ID NO:123.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vj1\_1 should be approximately 2895 bp.

The nucleotide sequence disclosed herein for vj1\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vj1\_1 demonstrated at least some similarity with sequences identified as AA410352 (zv11f01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753337 5', mRNA sequence). Based upon sequence similarity, vj1\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vj1\_1 protein sequence centered around amino acid 70 of SEQ ID NO:14. The nucleotide sequence of vj1\_1 indicates that it may contain repetitive elements.

Clone "vl1\_1"

A polynucleotide of the present invention has been identified as clone "vl1\_1". vl1\_1 was isolated from a human fetal cartilage cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vl1\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vl1\_1 protein").

The nucleotide sequence of vl1\_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the vl1\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 187 to 199 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 200. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should  
10 the predicted leader/signal sequence not be separated from the remainder of the vl1\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vl1\_1 should be approximately 1936 bp.

The nucleotide sequence disclosed herein for vl1\_1 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vl1\_1 demonstrated at least some similarity with sequences identified as AA464362 (zx81b12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810143 5', mRNA sequence), M90089 (Mouse inositol 1,4,5-triphosphate receptor mRNA sequence), and T21689 (Human gene signature HUMGS03131; standard; cDNA  
20 to mRNA). The predicted amino acid sequence disclosed herein for vl1\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vl1\_1 protein demonstrated at least some similarity to the sequence identified as U80846 (partial CDS [Caenorhabditis elegans]). Based upon sequence similarity, vl1\_1 proteins and each similar protein or peptide may share at least  
25 some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vl1\_1 protein sequence, one centered around amino acid 192 and another around amino acid 234 of SEQ ID NO:16.

vl1\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 37 kDa was detected in membrane fractions using SDS  
30 polyacrylamide gel electrophoresis.

Clone "vk2\_1"

A polynucleotide of the present invention has been identified as clone "vk2\_1". vk2\_1 was isolated from a human adult brain cDNA library (enriched for G-protein-coupled receptors) and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vk2\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vk2\_1 protein").

The nucleotide sequence of vk2\_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vk2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 10 to 22 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vk2\_1 protein. Basepairs 416 to 418 of SEQ ID NO:17 may represent the site of an alternatively spliced exon that is not present in clone vk2\_1.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vk2\_1 should be approximately 1284 bp.

The nucleotide sequence disclosed herein for vk2\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vk2\_1 demonstrated at least some similarity with sequences identified as AA152101 (zl49f09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505289 3', mRNA sequence) and Q78696 (Sequence encoding therapeutic polypeptide from glioblastoma cell line; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vk2\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vk2\_1 protein demonstrated at least some similarity to the sequence identified as R66278 (Therapeutic polypeptide from glioblastoma cell line). Based upon sequence similarity, vk2\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vk2\_1 protein sequence, one centered around amino acid 61 and another around amino acid 97 of SEQ ID NO:18.

Clone "vb21\_1"

A polynucleotide of the present invention has been identified as clone "vb21\_1". vb21\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb21\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb21\_1 protein").

The nucleotide sequence of vb21\_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb21\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 296 to 308 of SEQ ID NO:20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 309. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb21\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb21\_1 should be approximately 4159 bp.

The nucleotide sequence disclosed herein for vb21\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb21\_1 demonstrated at least some similarity with sequences identified as AA026150 (zj99c10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469170 3', mRNA sequence), T72108 (Human semaphorin Z gene; standard; cDNA to mRNA), U52840 (Human semaphorin F homolog), X97817 (M. musculus mRNA for semaphorin F), and X97818 (M. musculus mRNA for semaphorin G). The predicted amino acid sequence disclosed herein for vb21\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb21\_1 protein demonstrated at least some similarity to sequences identified as W19857 (Human semaphorin Z) and X97818 (semaphorin G [Mus musculus]). Semaphorins are important membrane proteins involved in axonal guidance in the embryonic stage, and may also have a role in nerve regeneration after injury. Based upon sequence similarity, vb21\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the vb21\_1 protein sequence, centered around amino acids 237, 523, 769, and 895 of SEQ ID NO:20, respectively.

Clone "vc35\_1"

A polynucleotide of the present invention has been identified as clone "vc35\_1". vc35\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc35\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc35\_1 protein").

The nucleotide sequence of vc35\_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc35\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 38 to 50 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 51. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc35\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc35\_1 should be approximately 3042 bp.

The nucleotide sequence disclosed herein for vc35\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc35\_1 demonstrated at least some similarity with sequences identified as AA532364 (nj12a08.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA clone IMAGE:986102, mRNA sequence), AF029343 (human protocadherin 68), and T22263 (Human gene signature HUMGS03835; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc35\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc35\_1 protein demonstrated at least some similarity to sequences identified as Y08715 (protocadherin-4 [Mus musculus]). Based upon sequence similarity, vc35\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vc36\_1"

A polynucleotide of the present invention has been identified as clone "vc36\_1". vc36\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vc36\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc36\_1 protein").

The nucleotide sequence of vc36\_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the vc36\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 24 to 36 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should  
10 the predicted leader/signal sequence not be separated from the remainder of the vc36\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc36\_1 should be approximately 1395 bp.

The nucleotide sequence disclosed herein for vc36\_1 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc36\_1 demonstrated at least some similarity with sequences identified as AA259070 (zs33c04.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE 686982 5', mRNA sequence) and W67508 (zd40f11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343149 3', mRNA sequence). Based upon sequence similarity, vc36\_1  
20 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vc36\_1 indicates that it may contain repetitive elements.

#### Clone "vc38\_1"

A polynucleotide of the present invention has been identified as clone "vc38\_1".  
25 vc38\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc38\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc38\_1 protein").

The nucleotide sequence of vc38\_1 as presently determined is reported in SEQ ID  
30 NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc38\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc38\_1 should be approximately 2468 bp.



The nucleotide sequence disclosed herein for vc38\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc38\_1 demonstrated at least some similarity with sequences identified as AF037400 (neuropeptide Y/peptide YY receptor Ya [Danio rerio]). Motifs analysis and profile hidden markov model analysis of the predicted vc38\_1 protein both reveal the presence of the G-protein-coupled receptor signature. G-protein-coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants, and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Most G-protein-coupled receptors lack a signal peptide, as does the predicted vc38\_1 protein. Based upon sequence similarity, vc38\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts seven potential transmembrane domains within the vc38\_1 protein sequence, centered around amino acids 60, 90, 130, 170, 225, 280, and 318 of SEQ ID NO:26, respectively.

vc38\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 71 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "vc39\_1"

A polynucleotide of the present invention has been identified as clone "vc39\_1". vc39\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc39\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc39\_1 protein").

The nucleotide sequence of vc39\_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc39\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 2 to 14 of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc39\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc39\_1 should be approximately 2048 bp.

The nucleotide sequence disclosed herein for vc39\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc39\_1 demonstrated at least some similarity with sequences identified as AA631722 (np79d04.s1 NCI\_CGAP\_Pr2 Homo sapiens cDNA clone IMAGE:1132519 similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, vc39\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vc39\_1 protein sequence centered around amino acid 40 of SEQ ID NO:28. The nucleotide sequence of vc39\_1 indicates that it may contain an Alu/SVA repetitive element.

Clone "vc40\_1"

A polynucleotide of the present invention has been identified as clone "vc40\_1". vc40\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc40\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc40\_1 protein").

The nucleotide sequence of vc40\_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc40\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 19 to 31 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc40\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc40\_1 should be approximately 2297 bp.

The nucleotide sequence disclosed herein for vc40\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc40\_1 demonstrated at least some similarity with sequences

identified as AA143014 (zl48g04.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505206 5', mRNA sequence) and T20006 (Human gene signature HUMGS01143; standard; cDNA to mRNA). Based upon sequence similarity, vc40\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer  
5 program predicts three additional potential transmembrane domains within the vc40\_1 protein sequence, centered around amino acids 101, 136, and 182 of SEQ ID NO:30, respectively.

Clone "vc46\_1"

10 A polynucleotide of the present invention has been identified as clone "vc46\_1". vc46\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc46\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc46\_1 protein").

15 The nucleotide sequence of vc46\_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc46\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 10 to 22 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature  
20 amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc46\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 vc46\_1 should be approximately 2938 bp.

The nucleotide sequence disclosed herein for vc46\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc46\_1 demonstrated at least some similarity with sequences identified as AA029404 (ze94e06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA  
30 clone 366658 5', mRNA sequence) and AQ071029 (human genomic fragment). Based upon sequence similarity, vc46\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vc46\_1 protein sequence, one centered around amino acid 70 and another around amino acid 130 of SEQ ID NO:32.

vc46\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 19 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "vc49\_1"

A polynucleotide of the present invention has been identified as clone "vc49\_1". vc49\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc49\_1 is a full-length clone, including the  
10        entire coding sequence of a secreted protein (also referred to herein as "vc49\_1 protein").

The nucleotide sequence of vc49\_1 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc49\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 14 to 26  
15        of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc49\_1 protein.

20        The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc49\_1 should be approximately 3471 bp.

The nucleotide sequence disclosed herein for vc49\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc49\_1 demonstrated at least some similarity with sequences  
25        identified as AI075929 (ov46h11.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE 1640421 3' similar to TR Q63418 Q63418 PROTOCADHERIN-3; mRNA sequence), I79964 (Sequence 109 from patent US 5708143), and T03572 (Human protocadherin pc3 coding sequence; standard; cDNA). The predicted amino acid sequence disclosed herein for vc49\_1 was searched against the GenPept and GeneSeq amino acid sequence databases  
30        using the BLASTX search protocol. The predicted vc49\_1 protein demonstrated at least some similarity to sequences identified as L43592 (protocadherin-3 [Rattus norvegicus]) and R86865 (Human protocadherin pc3). Based upon sequence similarity, vc49\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vc49\_1

protein sequence, one definite transmembrane domain centered around amino acid 700 and another possible transmembrane domain centered around amino acid 260 of SEQ ID NO:34. Profile hidden markov model and motifs analyses of the predicted vc49\_1 protein sequence have revealed it to contain five cadherin extracellular repeated domain signatures at amino acids 142 to 242, 251 to 347, 356 to 451, 460 to 561, and 576 to 671 of SEQ ID NO:34. Cadherins are a family of animal glyco-proteins responsible for calcium-dependent cell-cell adhesion. Cadherins preferentially interact with themselves in a homophilic manner in connecting cells; thus acting as both receptor and ligand. Structurally, cadherins are built of the following domains: a signal sequence, followed by a propeptide of about 130 residues, then an extracellular domain of around 600 residues, then a transmembrane region, and finally a C-terminal cytoplasmic domain of about 150 residues. The predicted vc49\_1 protein sequence almost exactly follows this structure (its cytoplasmic domain being approximately 100 amino acids). Clearly, vc49\_1 protein appears to represent a novel member of the cadherin superfamily.

#### Clone "vc50\_1"

A polynucleotide of the present invention has been identified as clone "vc50\_1". vc50\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc50\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc50\_1 protein").

The nucleotide sequence of vc50\_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc50\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. Amino acids 20 to 32 of SEQ ID NO:36 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc50\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc50\_1 should be approximately 3819 bp.

The nucleotide sequence disclosed herein for vc50\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vc50\_1 demonstrated at least some similarity with sequences identified as AA193122 (zr39d05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665769 5', mRNA sequence), T26031 (Human gene signature HUMGS08267; standard; cDNA to mRNA), Z31718 (H.sapiens gene for myelin protein zero), and Z99943 (Human DNA sequence from PAC 313L4 on chromosome 1q24). The predicted amino acid sequence disclosed herein for vc50\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc50\_1 protein demonstrated at least some similarity to the sequence identified as K03242 (rat P0 myelin prepeptide), L24893 (myelin protein zero [Homo sapiens]), and M62860 (mouse peripheral myelin protein). Based upon sequence similarity, vc50\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vc50\_1 protein sequence centered around amino acid 181 of SEQ ID NO:36.

vc50\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "vc51\_1"

A polynucleotide of the present invention has been identified as clone "vc51\_1". vc51\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc51\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc51\_1 protein").

The nucleotide sequence of vc51\_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc51\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 12 to 24 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc51\_1 protein. If the "G" residue at position 388 of SEQ ID NO:37 were deleted, two alternative potential vc51\_1 reading frames and predicted amino acid sequences that could be

encoded by basepairs 333 to 1310 of SEQ ID NO:37 and by basepairs 139 to 522 of SEQ ID NO:37 are reported in SEQ ID NO:124 and SEQ ID NO:125, respectively.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc51\_1 should be approximately 1992 bp.

5       The nucleotide sequence disclosed herein for vc51\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc51\_1 demonstrated at least some similarity with sequences identified as T21514 (Human gene signature HUMGS02887; standard; cDNA to mRNA) and W52782 (zd13h06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340571  
10 5', mRNA sequence). The predicted amino acid sequence disclosed herein for vc51\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc51\_1 protein demonstrated at least some similarity to sequences identified as U90716 (human cell surface protein HCAR), Y07593 (coxsackie and adenovirus receptor protein [Homo sapiens]), Y10320 (mouse coxsackie  
15 and adenovirus receptor homolog), and W14146 (Human A33 antigen). Based upon sequence similarity, vc51\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the vc51\_1 protein sequence centered around amino acids 17, 216, 260, and 373 of SEQ ID NO:38, respectively.

20

#### Clone "vc52\_1"

A polynucleotide of the present invention has been identified as clone "vc52\_1". vc52\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the  
25 amino acid sequence of the encoded protein. vc52\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc52\_1 protein").

The nucleotide sequence of vc52\_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc52\_1 protein corresponding  
30 to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 19 to 31 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the vc52\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc52\_1 should be approximately 2018 bp.

5        The nucleotide sequence disclosed herein for vc52\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc52\_1 demonstrated at least some similarity with sequences identified as AA075627 (zm89a01.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545064 3', mRNA sequence) and T24879 (Human gene signature  
10 HUMGS06985; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc52\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc52\_1 protein demonstrated at least some similarity to sequences identified as AL021890 (putative protein [Arabidopsis thaliana]), L47993 (ORF YJR072c [Saccharomyces cerevisiae]), and U10402  
15 (undefined protein [Caenorhabditis elegans]). Based upon sequence similarity, vc52\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vc52\_1 protein sequence centered around amino acid 145 of SEQ ID NO:40.

vc52\_1 protein was expressed in a COS cell expression system, and an expressed  
20 protein band of approximately 44 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "vc33\_1"

A polynucleotide of the present invention has been identified as clone "vc33\_1".  
25 vc33\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc33\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc33\_1 protein").

The nucleotide sequence of vc33\_1 as presently determined is reported in SEQ ID  
30 NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc33\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 99 to 111 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 112. Due to the hydrophobic nature of the



predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc33\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
5 vc33\_1 should be approximately 2877 bp.

The nucleotide sequence disclosed herein for vc33\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc33\_1 demonstrated at least some similarity with sequences identified as AA846599 (aj97g02.s1 Soares parathyroid tumor NbHPA Homo sapiens  
10 cDNA clone IMAGE:1404434 3' similar to gb:M95549 SODIUM/GLUCOSE COTRANSPORTER-LIKE (HUMAN); mRNA sequence), M95549 (Homo sapiens sodium/glucose cotransporter-like protein mRNA, complete cds), and Q89779 (Cotransporter protein SNST1 cDNA; standard; cDNA). The predicted amino acid sequence disclosed herein for vc33\_1 was searched against the GenPept and GeneSeq  
15 amino acid sequence databases using the BLASTX search protocol. The predicted vc33\_1 protein demonstrated at least some similarity to sequences identified as M95549 (sodium/glucose cotransporter-like protein [Homo sapiens]) and R73593 (Cotransporter protein SNST1). Based upon sequence similarity, vc33\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts  
20 three additional potential transmembrane domains within the vc33\_1 protein sequence, centered around amino acids 186, 260, and 324 of SEQ ID NO:42, respectively.

vc33\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 45 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

25

#### Clone "vc34\_1"

A polynucleotide of the present invention has been identified as clone "vc34\_1". vc34\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the  
30 amino acid sequence of the encoded protein. vc34\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc34\_1 protein").

The nucleotide sequence of vc34\_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc34\_1 protein corresponding

to the foregoing nucleotide sequence is reported in SEQ ID NO:44. Amino acids 4 to 16 of SEQ ID NO:44 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc34\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc34\_1 should be approximately 3062 bp.

The nucleotide sequence disclosed herein for vc34\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc34\_1 demonstrated at least some similarity with sequences identified as AA927558 (om71e04.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE 1552638 3', mRNA sequence) and U79281 (Human clone 23588 mRNA sequence). Based upon sequence similarity, vc34\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vc34\_1 protein sequence, one centered around amino acid 251 and another around amino acid 283 of SEQ ID NO:44.

vc34\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 72 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "vc47\_1"

A polynucleotide of the present invention has been identified as clone "vc47\_1". vc47\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc47\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc47\_1 protein").

The nucleotide sequence of vc47\_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc47\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 93 to 105 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 106. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the vc47\_1 protein.

Another potential vc47\_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 1047 to 1322 of SEQ ID NO:45 is reported in SEQ ID NO:126. Amino acids 11 to 23 of SEQ ID NO:126 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:126.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc47\_1 should be approximately 3676 bp.

The nucleotide sequence disclosed herein for vc47\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc47\_1 demonstrated at least some similarity with sequences identified as AA339320 (EST44392 Fetal brain I Homo sapiens cDNA 5' end, mRNA sequence) and R02462 (ye82h04.r1 Homo sapiens cDNA clone 124279 5'). Based upon sequence similarity, vc47\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vc47\_1 indicates that it may contain one or more of the following repetitive elements: Alu, L1MB7.

#### Clone "vc54\_1"

A polynucleotide of the present invention has been identified as clone "vc54\_1". vc54\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc54\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc54\_1 protein").

The nucleotide sequence of vc54\_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc54\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 33 to 45 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 46. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the vc54\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc54\_1 should be approximately 2083 bp.

5       The nucleotide sequence disclosed herein for vc54\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc54\_1 demonstrated at least some similarity with sequences identified as AF007152 (Homo sapiens clone 23649 and 23755 unknown mRNA, partial cds), Q76901 (Human genome fragment (Preferred); standard; DNA), and T46905 (EST014  
10 BL29 Burkitt's lymphoma, Pascalis Sideras Homo sapiens cDNA clone BL29-14 5', mRNA sequence). The predicted amino acid sequence disclosed herein for vc54\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc54\_1 protein demonstrated at least some similarity to the sequence identified as AF007152 (unknown [Homo sapiens]). Based upon sequence  
15 similarity, vc54\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vc54\_1 protein sequence, one centered around amino acid 220 and another around amino acid 247 of SEQ ID NO:48.

vc54\_1 protein was expressed in a COS cell expression system, and an expressed  
20 protein band of approximately 44 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "vc57\_1"

A polynucleotide of the present invention has been identified as clone "vc57\_1".  
25 vc57\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc57\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc57\_1 protein").

The nucleotide sequence of vc57\_1 as presently determined is reported in SEQ ID  
30 NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc57\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 15 to 27 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the

predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc57\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
5 vc57\_1 should be approximately 2564 bp.

The nucleotide sequence disclosed herein for vc57\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc57\_1 demonstrated at least some similarity with sequences identified as AA156231 (zl50a11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA  
10 clone 505340 3', mRNA sequence). The predicted amino acid sequence disclosed herein for vc57\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc57\_1 protein demonstrated at least some similarity to the sequence identified as U41635 (OS-9 precursor [Homo sapiens]). Based upon sequence similarity, vc57\_1 proteins and each similar protein or peptide may  
15 share at least some activity.

vc57\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 51 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### 20 Clone "ve13\_1"

A polynucleotide of the present invention has been identified as clone "ve13\_1". ve13\_1 was isolated from a human adult brain (Alzheimer's hippocampus level 7) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ve13\_1 is a full-  
25 length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ve13\_1 protein").

The nucleotide sequence of ve13\_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ve13\_1 protein corresponding  
30 to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 551 to 563 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 564. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the ve13\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ve13\_1 should be approximately 3046 bp.

- 5        The nucleotide sequence disclosed herein for ve13\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ve13\_1 demonstrated at least some similarity with sequences identified as AA587395 (nn82h06.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA clone IMAGE:1090427 similar to contains element THR repetitive element; mRNA sequence)
- 10      and Q76778 (Human genome fragment (Preferred); standard; DNA). The predicted amino acid sequence disclosed herein for ve13\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ve13\_1 protein demonstrated at least some similarity to the sequence identified as U50828 (sel-1 gene product [Caenorhabditis elegans]). Based upon sequence similarity, ve13\_1 proteins
- 15      and each similar protein or peptide may share at least some activity.

#### Clone "ve16\_1"

- A polynucleotide of the present invention has been identified as clone "ve16\_1". ve16\_1 was isolated from a human adult brain (Alzheimer's hippocampus level 7) cDNA
- 20      library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ve16\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ve16\_1 protein").

- The nucleotide sequence of ve16\_1 as presently determined is reported in SEQ ID
- 25      NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ve16\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 14 to 26 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the
- 30      predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ve16\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ve16\_1 should be approximately 2033 bp.

The nucleotide sequence disclosed herein for ve16\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the databases. The nucleotide sequence of ve16\_1 indicates that it may contain one or more of the following repetitive elements:

5 Alu, MER.

Clone "vf3\_1"

A polynucleotide of the present invention has been identified as clone "vf3\_1". vf3\_1 was isolated from a human adult heart cDNA library and was identified as  
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vf3\_1 protein").

The nucleotide sequence of vf3\_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the vf3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 8 to 20 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should  
20 the predicted leader/signal sequence not be separated from the remainder of the vf3\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vf3\_1 should be approximately 2987 bp.

The nucleotide sequence disclosed herein for vf3\_1 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vf3\_1 demonstrated at least some similarity with sequences identified as Z78394 (H.sapiens mRNA, expressed sequence tag ICRFp507K11187 (5'), mRNA sequence). The predicted amino acid sequence disclosed herein for vf3\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
30 BLASTX search protocol. The predicted vf3\_1 protein demonstrated at least some similarity to the sequence identified as U41558 (K02B2.3 gene product [Caenorhabditis elegans]). Based upon sequence similarity, vf3\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two

additional potential transmembrane domains within the vf3\_1 protein sequence, one centered around amino acid 242 and another around amino acid 275 of SEQ ID NO:56.

vf3\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 39 kDa was detected in membrane fractions using SDS  
5 polyacrylamide gel electrophoresis.

#### Clone "vj2\_1"

A polynucleotide of the present invention has been identified as clone "vj2\_1". vj2\_1 was isolated from a human fetal brain (whole brain, enriched for G-protein-coupled  
10 receptors) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vj2\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vj2\_1 protein").

The nucleotide sequence of vj2\_1 as presently determined is reported in SEQ ID  
15 NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vj2\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 59 to 71 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 72. Due to the hydrophobic nature of the  
20 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vj2\_1 protein.

Another potential vj2\_1 reading frame and predicted amino acid sequence that could be encoded by basepairs 146 to 400 of SEQ ID NO:57 is reported in SEQ ID NO:127.  
25 The TopPredII computer program predicts two potential transmembrane domains within the amino acid sequence of SEQ ID NO:127.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vj2\_1 should be approximately 1762 bp.

The nucleotide sequence disclosed herein for vj2\_1 was searched against the  
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vj2\_1 demonstrated at least some similarity with sequences identified as N36445 (yx83c04.r1 Homo sapiens cDNA clone 268326 5'). Based upon sequence similarity, vj2\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane



domains within the vj2\_1 protein sequence, centered around amino acids 30, 67, and 90 of SEQ ID NO:58, respectively. The nucleotide sequence of vj2\_1 indicates that it may contain one or more repetitive elements.

5        Clone "vp7\_1"

A polynucleotide of the present invention has been identified as clone "vp7\_1". vp7\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp7\_1 is a full-length clone, including the  
10    entire coding sequence of a secreted protein (also referred to herein as "vp7\_1 protein").

The nucleotide sequence of vp7\_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp7\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 6 to 18  
15    of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp7\_1 protein. Another potential vp7\_1 reading frame and predicted amino acid sequence that  
20    could be encoded by basepairs 2071 to 2430 of SEQ ID NO:59 is reported in SEQ ID NO:128.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp7\_1 should be approximately 2638 bp.

The nucleotide sequence disclosed herein for vp7\_1 was searched against the  
25    GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp7\_1 demonstrated at least some similarity with sequences identified as N49433 (yv21e12.r1 Homo sapiens cDNA clone 243406 5') and Q63862 (AP2 sequence obtained by PCR for tumour specific DNA; standard; cDNA). Based upon sequence similarity, vp7\_1 proteins and each similar protein or peptide may share at least  
30    some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vp7\_1 protein sequence centered around amino acid 75 of SEQ ID NO:60. The nucleotide sequence of vp7\_1 indicates that it may contain one or more Alu repeat sequences.

Clone "vp8\_1"

A polynucleotide of the present invention has been identified as clone "vp8\_1". vp8\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp8\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp8\_1 protein").

The nucleotide sequence of vp8\_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp8\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 20 to 32 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp8\_1 protein. If two insertions of "C" residues were made in the nucleotide sequence of SEQ ID NO:61, one after the "A" at position 380 and another after the "G" at position 382, the resulting nucleotide sequence would be predicted to encode the amino acid sequence reported in SEQ ID NO:129.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp8\_1 should be approximately 1513 bp.

The nucleotide sequence disclosed herein for vp8\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp8\_1 demonstrated at least some similarity with sequences identified as AA284421 (zs59c10.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE 701778 5' similar to contains Alu repetitive element; mRNA sequence) and AC002086 (Human PAC clone DJ525N14 from Xq23, complete sequence). Based upon sequence similarity, vp8\_1 proteins and each similar protein or peptide may share at least some activity. Profile hidden markov model analysis reveals the presence of an SH2 domain in the predicted vp8\_1 protein (SEQ ID NO:62). SH2 domains function as regulatory modulators of intra-cellular signalling cascades by interacting with high affinity to phosphotyrosine-containing target peptides in a sequence-specific and strictly phosphorylation-dependent manner. The nucleotide sequence of vp8\_1 indicates that it may contain one or more Alu repeat sequences.

vp8\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 34 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "vb22\_1"

A polynucleotide of the present invention has been identified as clone "vb22\_1". vb22\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb22\_1 is a full-length clone, including the  
10    entire coding sequence of a secreted protein (also referred to herein as "vb22\_1 protein").

The nucleotide sequence of vb22\_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb22\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64.  
15    Another potential vb22\_1 reading frame and predicted amino acid sequence is encoded by basepairs 152 to 1006 of SEQ ID NO:63 and is reported in SEQ ID NO:130.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb22\_1 should be approximately 4176 bp.

The nucleotide sequence disclosed herein for vb22\_1 was searched against the  
20    GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb22\_1 demonstrated at least some similarity with sequences identified as L10335 (Homo sapiens neuroendocrine-specific protein C (NSP) mRNA, complete cds), N21304 (yx53f07.s1 Homo sapiens cDNA clone 265477 3' similar to SP:A60021 A60021 TROPOMYOSIN-RELATED PROTEIN, NEURONAL), and V23695  
25    (Human NSPLP protein A coding sequence; standard; cDNA). The predicted amino acid sequence disclosed herein for vb22\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb22\_1 protein demonstrated at least some similarity to sequences identified as L10333 (nueroendocrine-specific protein A [Homo sapiens]) and W53947 (Human NSPLP protein  
30    A). Based upon sequence similarity, vb22\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vb22\_1 protein sequence, one centered around amino acid 730 and another around amino acid 846 of SEQ ID NO:64. The nucleotide sequence of vb22\_1 appears to contain a short simple nucleotide repeat ("GGA") region.

Clone "vc48\_1"

A polynucleotide of the present invention has been identified as clone "vc48\_1". vc48\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc48\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc48\_1 protein").

The nucleotide sequence of vc48\_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc48\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 7 to 19 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc48\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc48\_1 should be approximately 3096 bp.

The nucleotide sequence disclosed herein for vc48\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc48\_1 demonstrated at least some similarity with sequences identified as AA292779 (zt56c06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726346 3', mRNA sequence). The predicted amino acid sequence disclosed herein for vc48\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc48\_1 protein demonstrated at least some similarity to sequences identified as AL031765 (Drosophila genomic product 22E5.z) and Z81058 (F11E6.e [Caenorhabditis elegans]). Based upon sequence similarity, vc48\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the vc48\_1 protein sequence, one centered around amino acid 39 and others around amino acids 69, 107 and 134 of SEQ ID NO:66, respectively. The nucleotide sequence of vc48\_1 appears to contain a simple nucleotide repeat ("AC") and one or more of the following repetitive elements: Alu and MIR.

Clone "vp3\_1"

A polynucleotide of the present invention has been identified as clone "vp3\_1". vp3\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp3\_1 protein").

The nucleotide sequence of vp3\_1 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 19 to 31 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp3\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp3\_1 should be approximately 552 bp.

The nucleotide sequence disclosed herein for vp3\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp3\_1 demonstrated at least some similarity with sequences identified as AA225045 (nc34c06.r1 NCI\_CGAP\_Pr2 Homo sapiens cDNA clone IMAGE 1010026, mRNA sequence), M18157 (Human glandular kallikrein gene, complete cds), and T35868 (Prostate-specific antigen gene partial sequence; standard; DNA). Based upon sequence similarity, vp3\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vc61\_1"

A polynucleotide of the present invention has been identified as clone "vc61\_1". vc61\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc61\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc61\_1 protein").

The nucleotide sequence of vc61\_1 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vc61\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 16 to 28 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc61\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc61\_1 should be approximately 3199 bp.

The nucleotide sequence disclosed herein for vc61\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc61\_1 demonstrated at least some similarity with sequences identified as AI028115 (ow51d09.x1 Soares\_parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone IMAGE 1650353 3' similar to gb S67859 TRANSCRIPTION INITIATION FACTOR IIE-ALPHA CHAIN (HUMAN); mRNA), V20913 (Human induced tumour protein cDNA), and Z99129 (Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene; Contains ESTs, STSs and GSSs, complete sequence). The predicted amino acid sequence disclosed herein for vc61\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc61\_1 protein demonstrated at least some similarity to sequences identified as W52812 (Human induced tumour protein) and Z99129 (dJ425C14.2 (Placental protein DIFF33 LIKE) [Homo sapiens]). The deduced vc61\_1 protein has amino acid similarity to human and mouse diff33 protein. Diff33 is a transmembrane protein which is overexpressed in testicular tumors from polyomavirus large T-antigen transgenic mice. Based upon sequence similarity, vc61\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts nine additional potential transmembrane domains within the vc61\_1 protein sequence, centered around amino acids 50, 100, 150, 210, 240, 270, 320, 390, and 430 of SEQ ID NO:70, respectively. The nucleotide sequence of vc61\_1 indicates that it may contain an Alu repetitive element.

Clone "vp15\_1"

A polynucleotide of the present invention has been identified as clone "vp15\_1". vp15\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp15\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp15\_1 protein").

The nucleotide sequence of vp15\_1 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp15\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72. Amino acids 4 to 16 of SEQ ID NO:72 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp15\_1 protein. If a "C" residue were inserted between nucleotides 458 and 459 of SEQ ID NO:71, nucleotides 44 to 568 of the resulting nucleotide sequence would encode a protein having an amino acid sequence reported as SEQ ID NO:131.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp15\_1 should be approximately 2033 bp.

The nucleotide sequence disclosed herein for vp15\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp15\_1 demonstrated at least some similarity with sequences identified as AI033082 (ow97g04.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE 1654806 3', mRNA sequence) and T21877 (Human gene signature HUMGS03418). The predicted amino acid sequence disclosed herein for vp15\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp15\_1 protein demonstrated at least some similarity to sequences identified as R45335 (Thrombomodulin analogue Q336N, Q365E) and U94333 (C1qR(p) [Homo sapiens]). The predicted vp15\_1 protein shows some amino acid similarity to multiple thrombomodulin analogues (such as GeneSeq accession number R45335), and shows some end-to-end similarity to GenPept accession number U94333, which is described as a "... human C1q/MBL/SPA receptor that mediates enhanced phagocytosis *in vitro*" (Nepomuceno *et al.*, 1997, *Immunity* 6(2): 119-129, which

is incorporated by reference herein). Based upon sequence similarity, vp15\_1 proteins and each similar protein or peptide may share at least some activity.

vp15\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in conditioned medium and  
5 membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "vp17\_1"

A polynucleotide of the present invention has been identified as clone "vp17\_1". vp17\_1 was isolated from a human adult prostate cDNA library and was identified as  
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp17\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp17\_1 protein").

The nucleotide sequence of vp17\_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the vp17\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 10 to 22 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
20 should the predicted leader/signal sequence not be separated from the remainder of the vp17\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp17\_1 should be approximately 3150 bp.

The nucleotide sequence disclosed herein for vp17\_1 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp17\_1 demonstrated at least some similarity with sequences identified as AI056890 (oz03g07.x1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE 1674300 3', mRNA sequence) and T64815 (Tumour suppressor activated pathway gene TSAP6). Based upon sequence similarity, vp17\_1 proteins and  
30 each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the vp17\_1 protein sequence, one centered around amino acid 50 and another around amino acid 80 of SEQ ID NO:74.



Clone "vp19\_1"

A polynucleotide of the present invention has been identified as clone "vp19\_1". vp19\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp19\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp19\_1 protein").

The nucleotide sequence of vp19\_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp19\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp19\_1 should be approximately 971 bp.

The nucleotide sequence disclosed herein for vp19\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp19\_1 demonstrated at least some similarity with sequences identified as AA716408 (zg64b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 398091 3', mRNA sequence) and T20711 (Human gene signature HUMGS01928). Based upon sequence similarity, vp19\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vp19\_1 protein sequence centered around amino acid 23 of SEQ ID NO:76; due to its hydrophobic nature, this region (amino acids 20 to 32) could also be a leader/signal sequence, with the mature protein beginning at amino acid 33 of SEQ ID NO:76.

Clone "vq1\_1"

A polynucleotide of the present invention has been identified as clone "vq1\_1". vq1\_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq1\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq1\_1 protein").

The nucleotide sequence of vq1\_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq1\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78. Amino acids 17 to 29

of SEQ ID NO:78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq1\_1 protein. If a "T" residue were inserted between nucleotides 332 and 333 of SEQ ID NO:77, nucleotides 54 to 496 of the resulting nucleotide sequence would encode a protein having an amino acid sequence reported as SEQ ID NO:132.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq1\_1 should be approximately 873 bp.

The nucleotide sequence disclosed herein for vq1\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq1\_1 demonstrated at least some similarity with sequences identified as No hits were found in the databases. The TopPredII computer program predicts an additional potential transmembrane domain within the vq1\_1 protein sequence, extending from about amino acid 36 to about amino acid 76 of SEQ ID NO:78. The nucleotide sequence of vq1\_1 indicates that it may contain an Alu repetitive element.

#### Clone "vp14\_1"

A polynucleotide of the present invention has been identified as clone "vp14\_1". vp14\_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp14\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp14\_1 protein").

The nucleotide sequence of vp14\_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp14\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 5 to 17 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp14\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp14\_1 should be approximately 1355 bp.

The nucleotide sequence disclosed herein for vp14\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp14\_1 demonstrated at least some similarity with sequences identified as AI052724 (oz27a12.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:1676542 3' similar to SW:YQJQ\_BACSU P54554 HYPOTHETICAL OXIDOREDUCTASE IN GLNQ-ANSR INTERGENIC REGION; mRNA sequence) and T20001 (Human gene signature HUMGS01138). The predicted amino acid sequence disclosed herein for vp14\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp14\_1 protein demonstrated at least some similarity to sequences identified as R61477 (Clavulanic acid dehydrogenase sequence) and Z99116 (similar to ketoacyl reductase [Bacillus subtilis]). The predicted vp14\_1 protein shows some amino acid similarity to various dehydrogenases due to the presence of a short-chain alcohol dehydrogenase family signature at amino acids 51 to 240 of SEQ ID NO:80, as detected by motifs and hidden markov model analysis. Based upon sequence similarity, vp14\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the vp14\_1 protein sequence, centered around amino acids 55, 195, 230, and 300 of SEQ ID NO:80, respectively.

#### Deposit of Clones

Clones vb11\_1, vb12\_1, vb14\_1, ve11\_1, vf2\_1, vg2\_1, vj1\_1, and vl1\_1 were deposited on August 20, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98846, from which each clone comprising a particular polynucleotide is obtainable.

Clone vk2\_1 was deposited on August 20, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98838, from which the vk2\_1 clone comprising a particular polynucleotide is obtainable.

Clones vb21\_1, vc35\_1, vc36\_1, vc38\_1, vc39\_1, vc40\_1, vc46\_1, vc49\_1, vc50\_1, vc51\_1, and vc52\_1 were deposited on September 2, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98862, from which each clone comprising a particular polynucleotide is obtainable.

Clones vc33\_1, vc34\_1, vc47\_1, vc54\_1, vc57\_1, ve13\_1, ve16\_1, vf3\_1, vj2\_1, vp7\_1, and vp8\_1 were deposited on September 22, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98886, from which each clone comprising a particular polynucleotide is obtainable.

Clones vb22\_1, vc48\_1, and vp3\_1 were deposited on October 16, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98933, from which each clone comprising a particular polynucleotide is obtainable.

Clones vc61\_1, vp15\_1, vp17\_1, vp19\_1, and vq1\_1 were deposited on December 23, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 207012, from which each clone comprising a particular polynucleotide is obtainable.

Clone vp14\_1 was deposited on December 23, 1998 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 207011, from which the vp14\_1 clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector

("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
20	vb11_1	SEQ ID NO:81
	vb12_1	SEQ ID NO:82
	vb14_1	SEQ ID NO:83
	ve11_1	SEQ ID NO:84
	vf2_1	SEQ ID NO:85
25	vg2_1	SEQ ID NO:86
	vj1_1	SEQ ID NO:87
	vl1_1	SEQ ID NO:88
	vk2_1	SEQ ID NO:89
	vb21_1	SEQ ID NO:90
30	vc35_1	SEQ ID NO:91
	vc36_1	SEQ ID NO:92
	vc38_1	SEQ ID NO:93
	vc39_1	SEQ ID NO:94
	vc40_1	SEQ ID NO:95

	vc46_1	SEQ ID NO:96
	vc49_1	SEQ ID NO:97
	vc50_1	SEQ ID NO:98
	vc51_1	SEQ ID NO:99
5	vc52_1	SEQ ID NO:100
	vc33_1	SEQ ID NO:101
	vc34_1	SEQ ID NO:102
	vc47_1	SEQ ID NO:103
	vc54_1	SEQ ID NO:104
10	vc57_1	SEQ ID NO:105
	ve13_1	SEQ ID NO:106
	ve16_1	SEQ ID NO:107
	vf3_1	SEQ ID NO:108
	vj2_1	SEQ ID NO:109
15	vp7_1	SEQ ID NO:110
	vp8_1	SEQ ID NO:111
	vb22_1	SEQ ID NO:112
	vc48_1	SEQ ID NO:113
	vp3_1	SEQ ID NO:114
20	vc61_1	SEQ ID NO:115
	vp15_1	SEQ ID NO:116
	vp17_1	SEQ ID NO:117
	vp19_1	SEQ ID NO:118
	vq1_1	SEQ ID NO:119
25	vp14_1	SEQ ID NO:120

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
  - (b) It should be designed to have a  $T_m$  of approx.  $80^\circ\text{C}$  (assuming  $2^\circ$  for each A or T and  $4^\circ$  for each G or C).
- 5 The oligonucleotide should preferably be labeled with  $\gamma\text{-}^{32}\text{P}$  ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated
- 10 by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately  $4\text{e}+6$  dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu\text{L}$  of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu\text{g}/\text{ml}$ . The culture should preferably be

15 grown to saturation at  $37^\circ\text{C}$ , and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100  $\mu\text{g}/\text{ml}$  and agar at 1.5% in a 150 mm petri dish when grown overnight at  $37^\circ\text{C}$ . Other

20 known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at  $65^\circ\text{C}$  for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100  $\mu\text{g}/\text{ml}$  of yeast RNA, and 10 mM EDTA (approximately

25 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to  $1\text{e}+6$  dpm/mL. The filter is then preferably incubated at  $65^\circ\text{C}$  with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed

30 by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at  $65^\circ\text{C}$  for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that



has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately  
5 labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences  
10 disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to  
15 identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense  
20 polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide  
25 molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* 391 (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* 95 (26): 15502-15507; and Sharp, 1999, *Genes Dev.* 13 (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have  
30 multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are

also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through  
5 deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination,  
10 preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for  
15 the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part  
20 or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of  
25 transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most  
30 preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are

proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

5           In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of*  
10 *Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX  
15 platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely  
20 used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length  
25 one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six,  
30 seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps.

The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuáñez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90%

identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and  
5 screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly  
10 stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,

5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or  
10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably  
15 linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined  
20 herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the  
25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).



Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to  
5 provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which  
10 are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by  
15 virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement,  
20 insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement,  
25 insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

#### USES AND BIOLOGICAL ACTIVITY

5           The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies  
10 or vectors suitable for introduction of DNA).

##### Research Uses and Utilities

          The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express  
15 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare  
20 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for  
25 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those  
30 described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine  
5 levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially  
10 binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent  
15 grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to  
20 Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein  
25 or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention  
30 can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10 Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- 20 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 25 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., *Proc. Natl. Acad. Sci. USA* 77:6091-6095, 1980; Weinberger et al., *Eur. J. Immun.* 11:405-411, 1981; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5       The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as  
10 described in Lenschow *et al.*, *Science* 257:789-792 (1992) and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15       Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.  
20 Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from  
25 the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and  
30 murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$



microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated  
 5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated  
 10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
 15 limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al.,  
 20 *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnoli et al.,  
 25 *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro*  
 30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995;
- 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others,
- 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993;
- 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25

#### Hematopoiesis Regulating Activity

- A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell
- 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

5

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,  
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as  
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal  
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue  
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in  
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting  
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

20 A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,  
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant  
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:



Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static  
5 conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### 10 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the  
15 inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic  
20 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to  
30 tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this  
5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells  
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas  
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed  
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the  
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block  
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic  
5 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another  
10 material or entity which is cross-reactive with such protein.

#### ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a  
15 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the  
20 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other  
25 agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor,  
30 thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in  
5 combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If  
10 administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical  
15 composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is  
20 administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.  
25 When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid  
30 form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

10 The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

25 The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

30 Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, 5 Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the 10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing 15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be 20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide 25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, *FEBS Lett.* 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful 30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where



abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5       For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably  
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the  
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical  
20 applications.

      The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium  
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other  
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions  
5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of  
10 carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to  
15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in  
20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to  
25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of  
30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such  
5 polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present  
10 invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:1;
- (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 683 to nucleotide 934;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vb11\_1 deposited with the ATCC under accession number 98846;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:1.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.

5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

- (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
  - (b) purifying said protein from the culture.
- 6. A protein produced according to the process of claim 5.
- 7. An isolated polynucleotide encoding the protein of claim 6.
- 8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846.
- 9. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:2;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb11\_1 deposited with the ATCC under accession number 98846;the protein being substantially free from other mammalian proteins.
- 10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
- 11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
- 12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:3;
  - (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 63 to nucleotide 482;
  - (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 201 to nucleotide 482;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb12\_1 deposited with the ATCC under accession number 98846;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb12\_1 deposited with the ATCC under accession number 98846;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb12\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;
- (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 1195 to nucleotide 1527;
- (c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 1468 to nucleotide 1527;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb14\_1 deposited with the ATCC under accession number 98846; the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:7;
- (b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 82 to nucleotide 294;
- (c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 109 to nucleotide 294;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ve11\_1 deposited with the ATCC under accession number 98846;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ve11\_1 deposited with the ATCC under accession number 98846;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.



17. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ve11\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:9;
- (b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 22 to nucleotide 468;
- (c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 118 to nucleotide 468;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vf2\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 124 to nucleotide 1641;
- (c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 262 to nucleotide 1641;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and

(c) the amino acid sequence encoded by the cDNA insert of clone vg2\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:13;

(b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 380 to nucleotide 892;

(c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 416 to nucleotide 892;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vj1\_1 deposited with the ATCC under accession number 98846;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

(f) the nucleotide sequence of a mature protein coding sequence of clone vj1\_1 deposited with the ATCC under accession number 98846;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone vj1\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:15;

(b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 62 to nucleotide 1057;

(c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 659 to nucleotide 1057;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vl1\_1 deposited with the ATCC under accession number 98846;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846;

(f) the nucleotide sequence of a mature protein coding sequence of clone vl1\_1 deposited with the ATCC under accession number 98846;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vl1\_1 deposited with the ATCC under accession number 98846;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:17;

- (b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 74 to nucleotide 529;
- (c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 140 to nucleotide 529;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vk2\_1 deposited with the ATCC under accession number 98838;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vk2\_1 deposited with the ATCC under accession number 98838;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vk2\_1 deposited with the ATCC under accession number 98838;

the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 174 to nucleotide 3170;
- (c) the nucleotide sequence of SEQ ID NO:19 from nucleotide 1098 to nucleotide 3170;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb21\_1 deposited with the ATCC under accession number 98862;
- the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 74 to nucleotide 1453;
- (c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 224 to nucleotide 1453;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc35\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc35\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees



C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
- (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc35\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
- (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 135 to nucleotide 368;
- (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 243 to nucleotide 368;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc36\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc36\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc36\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:25;
- (b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 370 to nucleotide 1662;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vc38\_1 deposited with the ATCC under accession number 98862;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc38\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc38\_1 deposited with the ATCC under accession number 98862;
- the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 105 to nucleotide 365;
- (c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 147 to nucleotide 365;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc39\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc39\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc39\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:29;

(b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 35 to nucleotide 1066;

(c) the nucleotide sequence of SEQ ID NO:29 from nucleotide 128 to nucleotide 1066;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc40\_1 deposited with the ATCC under accession number 98862;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc40\_1 deposited with the ATCC under accession number 98862;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc40\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:31;

(b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 38 to nucleotide 553;

(c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 104 to nucleotide 553;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc46\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 164 to nucleotide 2548;
- (c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 242 to nucleotide 2548;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc49\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc49\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc49\_1 deposited with the ATCC under accession number 98862; the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:35;
- (b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 150 to nucleotide 776;
- (c) the nucleotide sequence of SEQ ID NO:35 from nucleotide 246 to nucleotide 776;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:35.



45. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc50\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 139 to nucleotide 1308;
- (c) the nucleotide sequence of SEQ ID NO:37 from nucleotide 211 to nucleotide 1308;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc51\_1 deposited with the ATCC under accession number 98862;
- the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 21 to nucleotide 1142;
- (c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 114 to nucleotide 1142;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc52\_1 deposited with the ATCC under accession number 98862;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc52\_1 deposited with the ATCC under accession number 98862;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc52\_1 deposited with the ATCC under accession number 98862;

the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:41;

(b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 13 to nucleotide 1416;

(c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 346 to nucleotide 1416;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc33\_1 deposited with the ATCC under accession number 98886;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc33\_1 deposited with the ATCC under accession number 98886;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc33\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:43;

(b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 232 to nucleotide 1461;

(c) the nucleotide sequence of SEQ ID NO:43 from nucleotide 280 to nucleotide 1461;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc34\_1 deposited with the ATCC under accession number 98886;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc34\_1 deposited with the ATCC under accession number 98886;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc34\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:45;

- (b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 1922 to nucleotide 2350;
- (c) the nucleotide sequence of SEQ ID NO:45 from nucleotide 2237 to nucleotide 2350;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
- (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc47\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 111 to nucleotide 1337;
- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 246 to nucleotide 1337;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc54\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc54\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc54\_1 deposited with the ATCC under accession number 98886;
- the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 189 to nucleotide 1637;
- (c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 270 to nucleotide 1637;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc57\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc57\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees



C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vc57\_1 deposited with the ATCC under accession number 98886;
- the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 15 to nucleotide 1934;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 1704 to nucleotide 1934;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ve13\_1 deposited with the ATCC under accession number 98886;
- the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:53;
- (b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 240 to nucleotide 503;
- (c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 318 to nucleotide 503;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ve16\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ve16\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone ve16\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 11 to nucleotide 1063;

(c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 71 to nucleotide 1063;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vf3\_1 deposited with the ATCC under accession number 98886;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;

(f) the nucleotide sequence of a mature protein coding sequence of clone vf3\_1 deposited with the ATCC under accession number 98886;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone vf3\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:57;

(b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 542 to nucleotide 886;

(c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 755 to nucleotide 886;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone vj2\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vj2\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vj2\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:59;
- (b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 30 to nucleotide 344;
- (c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 84 to nucleotide 344;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp7\_1 deposited with the ATCC under accession number 98886; the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 23 to nucleotide 757;
- (c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 757;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp8\_1 deposited with the ATCC under accession number 98886;

the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:63;
- (b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 1048 to nucleotide 3726;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vb22\_1 deposited with the ATCC under accession number 98933;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:



- (a) the amino acid sequence of SEQ ID NO:64;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vb22\_1 deposited with the ATCC under accession number 98933;
- the protein being substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 134 to nucleotide 667;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 191 to nucleotide 667;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc48\_1 deposited with the ATCC under accession number 98933;

the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;
- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 65 to nucleotide 457;
- (c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 158 to nucleotide 457;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp3\_1 deposited with the ATCC under accession number 98933;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp3\_1 deposited with the ATCC under accession number 98933;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone vp3\_1 deposited with the ATCC under accession number 98933;
- the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 29 to nucleotide 1387;
- (c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 113 to nucleotide 1387;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc61\_1 deposited with the ATCC under accession number 207012;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number 207012;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc61\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:71;

(b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 44 to nucleotide 1513;

(c) the nucleotide sequence of SEQ ID NO:71 from nucleotide 92 to nucleotide 1513;

(d) the nucleotide sequence of SEQ ID NO:71 from nucleotide 1 to nucleotide 458;

(e) the nucleotide sequence of the full-length protein coding sequence of clone vp15\_1 deposited with the ATCC under accession number 207012;

(f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number 207012;

(g) the nucleotide sequence of a mature protein coding sequence of clone vp15\_1 deposited with the ATCC under accession number 207012;

(h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number 207012;

(i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and

(l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) the amino acid sequence of SEQ ID NO:72 from amino acid 1 to amino acid 139;

(c) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(d) the amino acid sequence encoded by the cDNA insert of clone vp15\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:73;
- (b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 348 to nucleotide 743;
- (c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 414 to nucleotide 743;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp17\_1 deposited with the ATCC under accession number 207012;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp17\_1 deposited with the ATCC under accession number 207012;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp17\_1 deposited with the ATCC under accession number 207012; the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 144 to nucleotide 461;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vp19\_1 deposited with the ATCC under accession number 207012;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp19\_1 deposited with the ATCC under accession number 207012;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
- (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp19\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:77;
- (b) the nucleotide sequence of SEQ ID NO:77 from nucleotide 54 to nucleotide 368;
- (c) the nucleotide sequence of SEQ ID NO:77 from nucleotide 141 to nucleotide 368;
- (d) the nucleotide sequence of SEQ ID NO:77 from nucleotide 51 to nucleotide 332;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone vq1\_1 deposited with the ATCC under accession number 207012;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;
- (g) the nucleotide sequence of a mature protein coding sequence of clone vq1\_1 deposited with the ATCC under accession number 207012;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:77.



87. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 93;
- (c) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (d) the amino acid sequence encoded by the cDNA insert of clone vq1\_1 deposited with the ATCC under accession number 207012;

the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 2 to nucleotide 1018;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 53 to nucleotide 1018;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp14\_1 deposited with the ATCC under accession number 207011;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp14\_1 deposited with the ATCC under accession number 207011;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp14\_1 deposited with the ATCC under accession number 207011;

the protein being substantially free from other mammalian proteins.

Fig. 1A

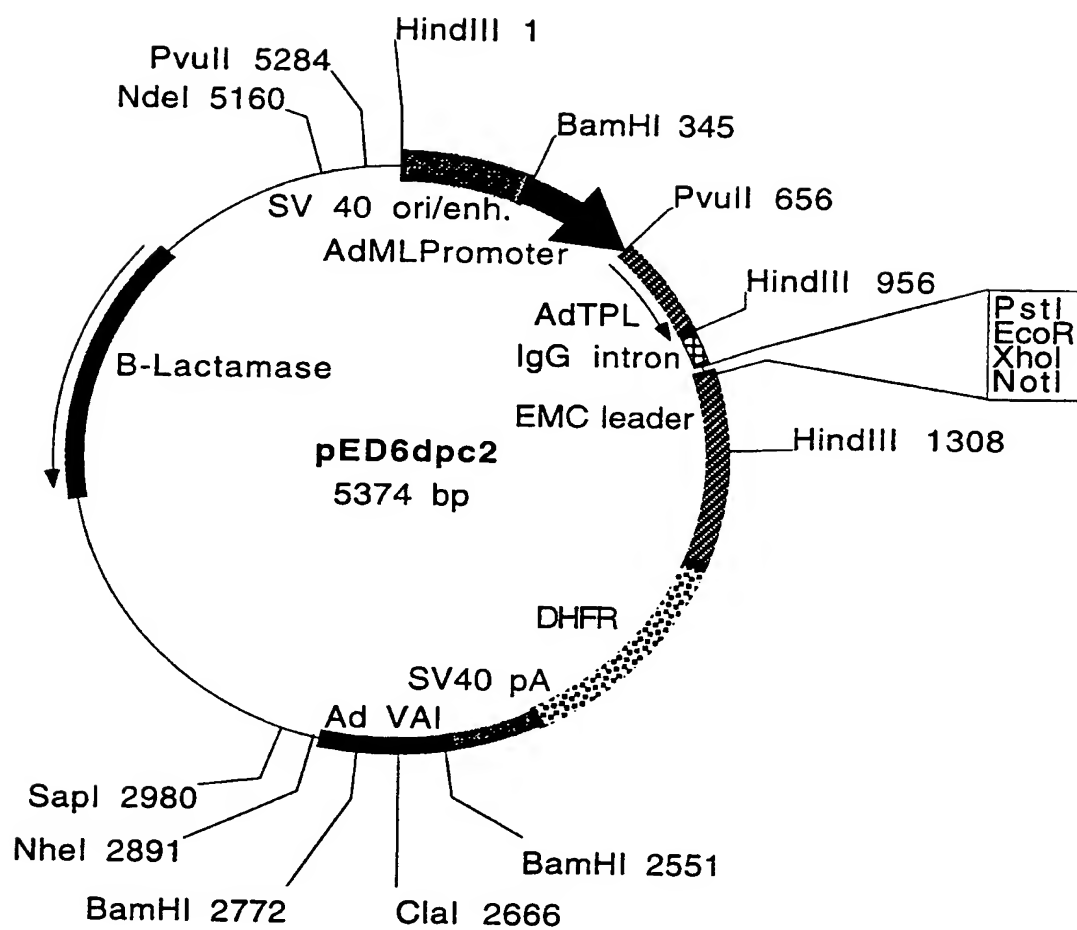
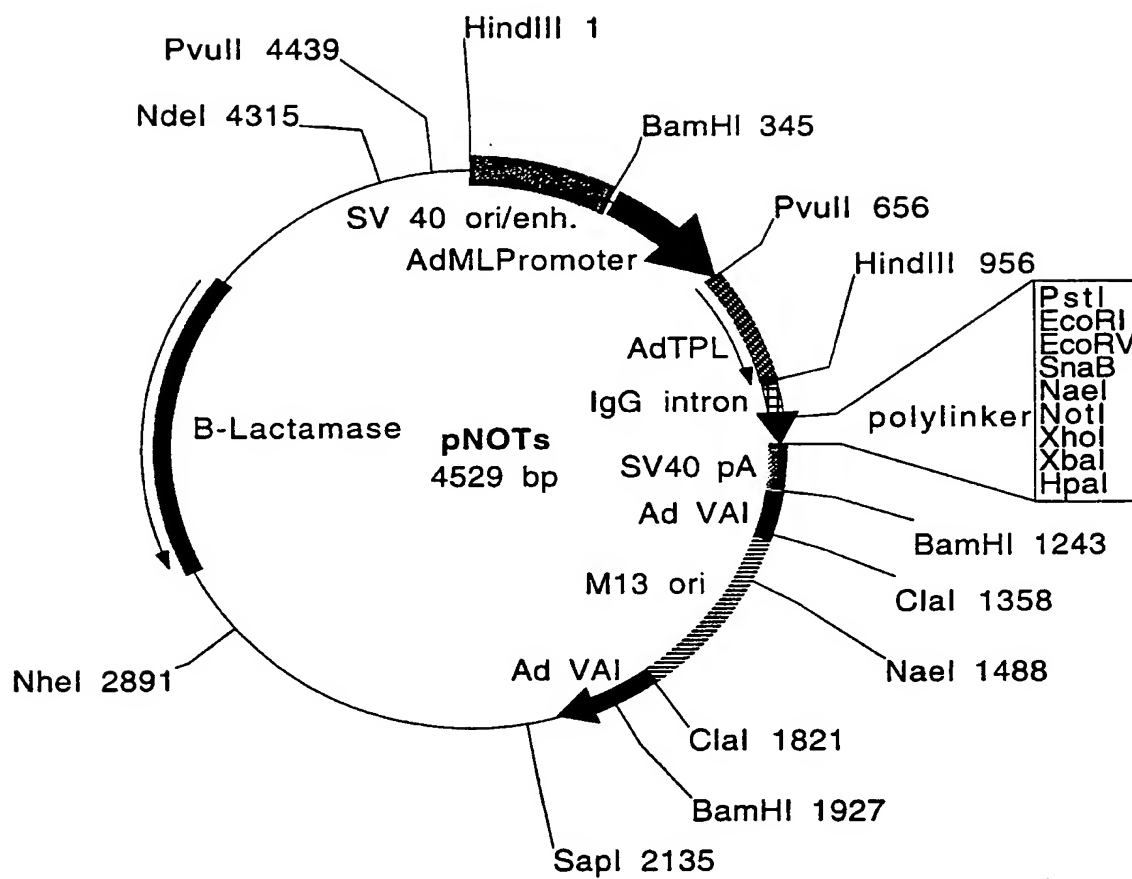


Fig. 1B



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<210> 8  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
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 Leu Trp Ser Phe Leu Ser Phe His Trp Leu Leu Pro Gln Glu Asp Ser  
 35 40 45  
 Ser Arg Leu Ser Ile Phe Pro Leu Arg Ala Gly Ser Pro Pro Gln Pro  
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 Ala Gln Ala Pro Pro Arg Ile  
 65 70

<210> 9  
 <211> 1100  
 <212> DNA  
 <213> Homo sapiens

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1100

&lt;210&gt; 10

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

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Ala Gly Arg Ala Ala Val Tyr Val Gly Leu Leu Gly Gly Ala Ala Ala  
 20 25 30

Cys Phe Thr Leu Ala Pro Ser Glu Gly Ala Phe Glu Glu Ala Leu Leu  
 35 40 45

Glu Ala Ser Gly Thr Leu Leu Leu Leu Ala Pro Ala Thr Arg Asn Arg  
 50 55 60

Gly Ser Trp Thr Trp Ala Ser Trp Val Ala Gly Gly Cys Trp Gly Pro  
 65 70 75 80

Gly Cys Ala Thr Ala Thr Ser Thr Thr Thr Asn Ser Cys Thr Cys Arg  
 85 90 95

Arg Ile Cys Gly Trp Ser Gly Pro Ser Ser Cys Ile Pro Arg Pro Thr  
 100 105 110

Ser Gly Ser Ser Met Arg Ser Thr Ser Leu Ser Cys Ser Pro Thr Ile  
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Arg Trp Thr Arg Arg Cys Gly Arg Ser Arg Ser Cys Arg Arg Arg Arg  
 130 135 140

Arg Thr Gly Ser Pro  
 145

&lt;210&gt; 11

&lt;211&gt; 2010

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

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<210> 12

<211> 506

<212> PRT

<213> Homo sapiens

<400> 12

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Ser Met Pro Pro Arg Arg Pro Trp Asp Arg Glu Ala Gly Thr Leu Gln
      20             25             30

Val Leu Gly Ala Leu Ala Val Leu Trp Leu Gly Ser Val Ala Leu Ile
 35             40             45

Cys Leu Leu Trp Gln Val Pro Arg Pro Pro Thr Trp Gly Gln Val Gln
 50             55             60

Pro Lys Asp Val Pro Arg Ser Trp Glu His Gly Ser Ser Pro Ala Trp
 65             70             75             80

Glu Pro Leu Glu Ala Glu Ala Arg Gln Gln Arg Asp Ser Cys Gln Leu
      85             90             95

Val Leu Val Glu Ser Ile Pro Gln Asp Leu Pro Ser Ala Ala Gly Ser
 100            105            110

Pro Ser Ala Gln Pro Leu Gly Gln Ala Trp Leu Gln Leu Leu Asp Thr
 115            120            125

Ala Gln Glu Ser Val His Val Ala Ser Tyr Tyr Trp Ser Leu Thr Gly
 130            135            140

Pro Asp Ile Gly Val Asn Asp Ser Ser Ser Gln Leu Gly Glu Ala Leu
 145            150            155            160

Leu Gln Lys Leu Gln Gln Leu Leu Gly Arg Asn Ile Ser Leu Ala Val
 165            170            175

Ala Thr Ser Ser Pro Thr Leu Ala Arg Thr Ser Thr Asp Leu Gln Val

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Thr	Arg	Gly	Val	Leu	His	Ser	Lys	Phe	Trp	Val	Val	Asp	Gly	Arg	His
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Ile	Tyr	Met	Gly	Ser	Ala	Asn	Met	Asp	Trp	Arg	Ser	Leu	Thr	Gln	Val
225					230					235					240
Lys	Glu	Leu	Gly	Ala	Val	Ile	Tyr	Asn	Cys	Ser	His	Leu	Ala	Gln	Asp
				245					250					255	
Leu	Glu	Lys	Thr	Phe	Gln	Thr	Tyr	Trp	Val	Leu	Gly	Val	Pro	Lys	Ala
			260					265					270		
Val	Leu	Pro	Lys	Thr	Trp	Pro	Gln	Asn	Phe	Ser	Ser	His	Phe	Asn	Arg
		275					280					285			
Phe	Gln	Pro	Phe	His	Gly	Leu	Phe	Asp	Gly	Val	Pro	Thr	Thr	Ala	Tyr
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Phe	Ser	Ala	Ser	Pro	Pro	Ala	Leu	Cys	Pro	Gln	Gly	Arg	Thr	Arg	Asp
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Arg	Tyr	Trp	Pro	Val	Leu	Asp	Asn	Ala	Leu	Arg	Ala	Ala	Ala	Phe	Gly
		355					360					365			
Lys	Gly	Val	Arg	Val	Arg	Leu	Leu	Val	Gly	Cys	Gly	Leu	Asn	Thr	Asp
	370					375					380				
Pro	Thr	Met	Phe	Pro	Tyr	Leu	Arg	Ser	Leu	Gln	Ala	Leu	Ser	Asn	Pro
385					390						395				400
Ala	Ala	Asn	Val	Ser	Val	Asp	Val	Lys	Val	Phe	Ile	Val	Pro	Val	Gly
			405						410					415	
Asn	His	Ser	Asn	Ile	Pro	Phe	Ser	Arg	Val	Asn	His	Ser	Lys	Phe	Met
			420					425					430		
Val	Thr	Glu	Lys	Ala	Ala	Tyr	Ile	Gly	Thr	Ser	Asn	Trp	Ser	Glu	Asp
		435					440					445			
Tyr	Phe	Ser	Ser	Thr	Ala	Gly	Val	Gly	Leu	Val	Val	Thr	Gln	Ser	Pro
	450					455						460			
Gly	Ala	Gln	Pro	Ala	Gly	Ala	Thr	Val	Gln	Glu	Gln	Leu	Arg	Gln	Leu
465					470					475					480
Phe	Glu	Arg	Asp	Trp	Ser	Ser	Arg	Tyr	Ala	Val	Gly	Leu	Asp	Gly	Gln
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505

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 <211> 2830  
 <212> DNA  
 <213> Homo sapiens

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<210> 14  
 <211> 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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Met Ile Val Val Ser Leu Ser Ala Ala Val Ala Ala Ala Phe Met
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Ala Lys Cys Arg Met Val Leu Ser Ser Arg Tyr Phe Cys Ser His Phe
          20             25             30

Val Met Ser Ala Ser Arg Ala Arg Ile Arg Ser Ser Phe Ser Arg Thr
      35             40             45

Ser Ser Arg Arg Ala Gly Ala Leu Tyr Ser Gly Met Leu Ala Gly Trp
      50             55             60

Pro Phe Pro Cys Phe Cys Trp Val Leu Ser Ala Ser Ser Ser Leu Ser
      65             70             75             80

Ser Gln Val Arg Ser Leu Arg Ser Ile Cys Ser Arg Phe Ser His Ala
          85             90             95

Asp Cys Ser Trp Val Arg Ala Cys Cys Ser Phe Ser Thr Phe Ser Thr
          100             105             110

Tyr Ala Cys Phe Ser Arg Asn Ser Ser Ser Ser Leu Met Thr Leu Ala
          115             120             125

Trp Ala Leu Leu Lys Ala Trp Ser Arg Ile Ser Met Cys Leu Arg Trp
          130             135             140

Ser Ser Leu Ala Val Arg Thr Ala Ala Asn Ser Ile Ser Asn Phe Ser
          145             150             155             160

Phe Ser Phe Lys Asn Ser Leu Phe Trp Glu Ala
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&lt;210&gt; 15

&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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&lt;210&gt; 16

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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Pro Glu Leu Ala Arg Arg Pro Ala Ser Met Leu Asn Trp Thr Thr Leu
          20                      25                      30

Gln Arg Leu Asn Ala Gly Gln Trp Phe Leu Lys Thr Asp Pro Phe Trp
          35                      40                      45

Thr Ala Ser Ser Leu Ser Pro Ser Asp His Arg Glu Ala Gln Asn Gln
          50                      55                      60

Ser Ile Cys Ser Leu Ala Glu Leu Leu Glu Leu Ala Lys Gly Asn Ala
          65                      70                      75                      80

Thr Leu Leu Leu Asn Leu Arg Asp Pro Pro Arg Glu His Pro Tyr Arg
          85                      90                      95

Ser Ser Phe Ile Asn Val Thr Leu Glu Ala Val Leu His Ser Gly Phe
          100                     105                     110

Pro Gln His Gln Val Met Trp Leu Pro Ser Arg Gln Arg Pro Leu Val
          115                     120                     125

Arg Lys Val Ala Pro Gly Phe Gln Gln Thr Ser Gly Ser Lys Glu Ala
          130                     135                     140

Val Ala Ser Leu Arg Arg Gly His Ile Gln Arg Leu Asn Leu Arg Tyr
          145                     150                     155                     160

Thr Gln Val Ser Arg Gln Glu Leu Arg Asp Tyr Ala Ser Trp Asn Leu
          165                     170                     175

Ser Val Asn Leu Tyr Thr Val Asn Ala Pro Trp Leu Phe Ser Leu Leu
          180                     185                     190

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 225 230 235 240  
 Ile Phe Val Leu Gln Lys Trp Arg Leu Gly Gly Ile Arg Ser Tyr Asn  
 245 250 255  
 Pro Glu Gln Ile Met Leu Ser Ala Ala Val Arg Arg Thr Ser Arg Asp  
 260 265 270  
 Val Ser Ile Met Lys Glu Lys Leu Ile Phe Ser Glu Ile Ser Asp Gly  
 275 280 285  
 Val Glu Val Ser Asp Val Leu Ser Val Cys Ser Asp Asn Ser Tyr Asp  
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 Thr Tyr Ala Asn Ser Thr Ala Thr Pro Val Gly Pro Arg Gly Gly Gly  
 305 310 315 320  
 Ser His Thr Lys Thr Leu Ile Glu Arg Ser Gly Arg  
 325 330

&lt;210&gt; 17

&lt;211&gt; 1170

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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&lt;210&gt; 18

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



&lt;400&gt; 18

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Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg  
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Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr  
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Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser  
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Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu  
 85 90 95

Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu  
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Arg Gly Gly Phe Leu Gly Ser Ser Gln Asp Arg Ser Ala Tyr Gln Thr  
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Ile Asp Ser Ala Glu Ala Pro Ala Asp Pro Phe Ala Val Pro Glu Gly  
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Arg Ser Gln Asp Ala Arg Gly Tyr  
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&lt;210&gt; 19

&lt;211&gt; 4144

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

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&lt;210&gt; 20

&lt;211&gt; 999

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

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Leu Cys Cys Leu Leu Leu Ser Phe Leu Pro Gln Glu Glu Cys Gln Asn

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Ser	Arg	Thr	Ile	Glu	Lys	Ile	Asn	Gly	Val	Ala	Arg	Cys	Pro	Tyr	Asp
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Pro	Arg	His	Asn	Ser	Thr	Ala	Val	Ile	Ser	Ser	Gln	Gly	Glu	Leu	Tyr
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Ala	Ala	Thr	Val	Ile	Asp	Phe	Ser	Gly	Arg	Asp	Pro	Ala	Ile	Tyr	Arg
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Ser	Leu	Gly	Ser	Gly	Pro	Pro	Leu	Arg	Thr	Ala	Gln	Tyr	Asn	Ser	Lys
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Thr	Val	Tyr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	Asn	Asp	Val	Gly	Gly
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His	Leu	Val	Val	Asp	Leu	Val	Gln	Ala	Lys	Asp	Thr	Leu	Tyr	His	Val
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Pro Pro Gly Arg Arg Glu Pro Leu Arg Ser Leu Arg Ile Leu His Ser		
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Ala Arg Ala Leu Phe Val Gly Leu Arg Asp Gly Val Leu Arg Val Pro		
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Leu Glu Arg Cys Ala Ala Tyr Arg Ser Gln Gly Ala Cys Leu Gly Ala		
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Arg Asp Pro Tyr Cys Gly Trp Asp Gly Lys Gln Gln Arg Cys Ser Thr		
420	425	430
Leu Glu Asp Ser Ser Asn Met Ser Leu Trp Thr Gln Asn Ile Thr Ala		
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Cys Pro Val Arg Asn Val Thr Arg Asp Gly Gly Phe Gly Pro Trp Ser		
450	455	460
Pro Trp Gln Pro Cys Glu His Leu Asp Gly Asp Asn Ser Gly Ser Cys		
465	470	475
Leu Cys Arg Ala Arg Ser Cys Asp Ser Pro Arg Pro Arg Cys Gly Gly		
485	490	495
Leu Asp Cys Leu Gly Pro Ala Ile His Ile Ala Asn Cys Ser Arg Asn		
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Gly Ala Trp Thr Pro Trp Ser Ser Trp Ala Leu Cys Ser Thr Ser Cys		
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Gly Ile Gly Phe Gln Val Arg Gln Arg Ser Cys Ser Asn Pro Ala Pro		
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Arg His Gly Gly Arg Ile Cys Val Gly Lys Ser Arg Glu Glu Arg Phe		
545	550	555
Cys Asn Glu Asn Thr Pro Cys Pro Val Pro Ile Phe Trp Ala Ser Trp		
565	570	575
Gly Ser Trp Ser Lys Cys Ser Ser Asn Cys Gly Gly Gly Met Gln Ser		
580	585	590
Arg Arg Arg Ala Cys Glu Asn Gly Asn Ser Cys Leu Gly Cys Gly Val		
595	600	605
Glu Phe Lys Thr Cys Asn Pro Glu Gly Cys Pro Glu Val Arg Arg Asn		
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Thr Pro Trp Thr Pro Trp Leu Pro Val Asn Val Thr Gln Gly Gly Ala		
625	630	635
Arg Gln Glu Gln Arg Phe Arg Phe Thr Cys Arg Ala Pro Leu Ala Asp		
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17

980

985

990

Gln Arg Cys Phe Pro Asn Ser  
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<211> 2820  
<212> DNA  
<213> Homo sapiens

<400> 21  
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 <211> 460  
 <212> PRT  
 <213> Homo sapiens

<400> 22

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Gly Ala Ile Cys Ala Val Leu Leu Val Ile Met Val Leu Phe Ala Thr
          35             40             45

Arg Cys Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys Arg Val
 50             55             60

Ala Glu Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln Ile
 65             70             75             80

His Lys Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu Pro
          85             90             95

Ile Arg Ser His His Arg Ser Ser Pro Ser Ser Ser Pro Thr Leu Glu
          100            105            110

Arg Gly Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser Leu
          115            120            125

Asn Ser Leu Val Thr Ile Ser Ser Asn His Val Pro Glu Asn Phe Ser
          130            135            140

Leu Glu Leu Thr His Ala Thr Pro Ala Val Glu Val Ser Gln Leu Leu
          145            150            155            160

Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly
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Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys
          180            185            190

Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser
          195            200            205

Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu
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Gly Phe Ser Asp Leu Phe Leu Thr Asp Gly Arg Ile Pro Ala Ala Met
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Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His Ser Asp Gln Cys
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Trp Met Pro Pro Leu Pro Ser Pro Ser Ser Asp Tyr Arg Ser Asn Met
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 Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp Thr Tyr Ser Glu Cys Ser  
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 355 360 365  
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 405 410 415  
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 450 455 460

&lt;210&gt; 23

&lt;211&gt; 1219

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

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aaaaaaaaa aaaaaaaaaa

1219

&lt;210&gt; 24

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

Met Pro Phe Thr Leu Gly Asn Leu Arg Ala Ile Leu Gly Ser Asn Pro  
 1 5 10 15

Thr Pro Leu Cys Ser Arg Pro His Leu Trp Leu Ser Leu Trp Ala Gln  
 20 25 30

Pro Leu Gln Pro Ser Arg Ser Pro Thr Ala Ala Ser Cys Leu His Cys  
 35 40 45

Arg Leu Arg Lys Leu Gln Leu Pro Asp Pro Glu Val Pro Leu Leu Pro  
 50 55 60

Ser Val Gly Lys Ser Leu Lys Glu Leu Ala Ser Arg Phe Leu  
 65 70 75

&lt;210&gt; 25

&lt;211&gt; 2411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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aaaaaaaaa a 2411

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<210> 26

<211> 431

<212> PRT

<213> Homo sapiens

<400> 26

```

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
  1              5              10              15

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```

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
              20              25              30

```

```

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
              35              40              45

```

```

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
  50              55              60

```

```

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
  65              70              75              80

```

```

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
              85              90              95

```

```

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
              100             105             110

```

```

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
              115             120             125

```

```

Val Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
              130             135             140

```

```

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
              145             150             155             160

```

```

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
              165             170             175

```

```

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
              180             185             190

```

```

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
              195             200             205

```

```

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
              210             215             220

```

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
 225 230 235 240  
 Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
 245 250 255  
 His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val  
 260 265 270  
 Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
 275 280 285  
 Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
 290 295 300  
 Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
 305 310 315 320  
 Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
 325 330 335  
 Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
 340 345 350  
 Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
 355 360 365  
 Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
 370 375 380  
 Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
 385 390 395 400  
 Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu  
 405 410 415  
 Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
 420 425 430

&lt;210&gt; 27

&lt;211&gt; 1945

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

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 cacttgctgt gaccttatac atgttgggggt ttgctcttaa agaggagagc aggaagaaag 300  
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 aggatttaag tttctcttta aaaattgcac tgaagaaagg cggggcgcggt tggtctcccc 480  
 tgtaatccca gcgcttttggg aggcgagggc ggggggatca cgaggtcaag agatcgagac 540  
 catcctggcc aacatggtga aaccccgctc ctaataaaaa tacaaaaatt agccgggcat 600  
 ggtgacgtgc acctgtagtc ccagctacta gataggctga ggcaggagaa ttgcttgaat 660  
 ccgggagggc gaggttgagc tgagccgaga tcgtgccact gaactccaac ctgccaatag 720  
 agcgagactc cgtctcaaaa aaaaaaaaaa aaaagaaaga aatagcattg aagaaaatac 780  
 cgcacatcag aggaaagcct attttctgca tgggtgtcttt tcaaagatag aatatttgaa 840

```

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cttccctttc tgcgccagc ttttgggtga aggggtgattt ctactagaca catctgtgct 1020
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tttgttgaac agaaacccaa ataaatttca aaatgttaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaa 1945

```

&lt;210&gt; 28

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

Met Leu Ser Tyr Leu Leu Ser Met Val Thr Phe Leu Arg Thr Ser Arg
  1             5             10             15

```

```

Val Gln Phe Leu Leu Ala Glu Arg Phe Ser Phe Ser Met Pro Tyr Gly
          20             25             30

```

```

Cys Asp Ser Asn Glu Gly Ser His Ser Phe Ser Trp Leu Pro Leu Ala
          35             40             45

```

```

Val Thr Leu Tyr Met Leu Gly Phe Ala Leu Lys Glu Glu Ser Arg Lys
          50             55             60

```

```

Lys Gly Trp Phe Gln Lys Pro Arg Gly Ser Ala Val Asp Ala Tyr Ile
          65             70             75             80

```

```

Leu Ser Arg Ser Pro Gln Ser
          85

```

&lt;210&gt; 29

&lt;211&gt; 2184

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

```

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gctctacaag ggcctctgt cgaagagcct tctgctggtc cccagtgcct tctccctcct 120
gctcgccctc ctctgcctc actgccagaa gctctttgtg tatgaccttc acgcagtcaa 180
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```

&lt;210&gt; 30

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

```

Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
  1                      5                      10                     15

Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
          20                      25                     30

Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val
          35                      40                     45

Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
          50                      55                     60

Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
          65                      70                     75                     80

Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
          85                      90                     95

Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
          100                     105                    110

Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
          115                     120                    125

Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser

```

130	135	140
Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr		
145	150	155 160
Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly		
	165	170 175
Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys		
	180	185 190
Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser		
	195	200 205
Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser		
	210	215 220
Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp		
225	230	235 240
Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe		
	245	250 255
Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met		
	260	265 270
Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val		
	275	280 285
Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu		
	290	295 300
Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg		
305	310	315 320
Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val		
	325	330 335
Ala Thr Asn Phe Leu Leu Gln His		
	340	

&lt;210&gt; 31

&lt;211&gt; 2880

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

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```

```

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 <212> PRT  
 <213> Homo sapiens

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 Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe  
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 Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe  
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Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln  
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 Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn  
 115 120 125  
 Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser  
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 <211> 3406  
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&lt;210&gt; 34

&lt;211&gt; 795

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

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Phe Leu Val Met Glu Glu Leu Gln Ser Gly Ser Phe Val Gly Asn Leu
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Ala Lys Thr Leu Gly Leu Glu Val Ser Glu Leu Ser Ser Arg Gly Ala
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Arg Val Val Ser Asn Asp Asn Lys Glu Cys Leu Gln Leu Asp Thr Asn
      65             70             75             80

Thr Gly Asp Leu Leu Leu Arg Glu Met Leu Asp Arg Glu Glu Leu Cys
      85             90             95

Gly Ser Asn Glu Pro Cys Val Leu Tyr Phe Gln Val Leu Met Lys Asn
      100            105            110

Pro Thr Gln Phe Leu Gln Ile Glu Leu Gln Val Arg Asp Ile Asn Asp
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His Ser Pro Val Phe Leu Glu Lys Glu Met Leu Leu Glu Ile Pro Glu
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Asn Ser Pro Val Gly Ala Val Phe Leu Leu Glu Ser Ala Lys Asp Leu
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Asp Val Gly Ile Asn Ala Val Lys Ser Tyr Thr Ile Asn Pro Asn Ser
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&lt;210&gt; 35

&lt;211&gt; 3809

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

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 <213> Homo sapiens

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<210> 37  
 <211> 1954

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

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&lt;210&gt; 38

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
      20                      25                     30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
      35                      40                     45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
      50                      55                     60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
      65                      70                     75                     80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

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85					90					95				
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Asn Val Gln	Asp Lys Gln	Gly Lys Ser	Arg Gly His	Ser Ile Lys Thr										
	130		135		140									
Leu Glu Leu	Asn Val Leu	Val Pro Pro	Ala Pro Pro	Ser Cys Arg Leu										
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Gln Gly Val	Pro His Val	Gly Ala Asn	Val Thr Leu	Ser Cys Gln Ser										
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Pro Arg Ser	Lys Pro Ala	Val Gln Tyr	Gln Trp Asp	Arg Gln Leu Pro										
	180		185		190									
Ser Phe Gln	Thr Phe Phe	Ala Pro Ala	Leu Asp Val	Ile Arg Gly Ser										
	195		200		205									
Leu Ser Leu	Thr Asn Leu	Ser Ser Ser	Met Ala Gly	Val Tyr Val Cys										
	210		215		220									
Lys Ala His	Asn Glu Val	Gly Thr Ala	Gln Cys Asn	Val Thr Leu Glu										
	225		230		235							240		
Val Ser Thr	Gly Pro Gly	Ala Ala Val	Val Ala Gly	Ala Val Val Gly										
	245		250		255									
Thr Leu Val	Gly Leu Gly	Leu Leu Ala	Gly Leu Val	Leu Leu Tyr His										
	260		265		270									
Arg Arg Gly	Lys Ala Leu	Glu Glu Pro	Ala Asn Asp	Ile Lys Glu Asp										
	275		280		285									
Ala Ile Ala	Pro Arg Thr	Leu Pro Trp	Pro Lys Ser	Ser Asp Thr Ile										
	290		295		300									
Ser Lys Asn	Gly Thr Leu	Ser Ser Val	Thr Ser Ala	Arg Ala Leu Arg										
	305		310		315							320		
Pro Pro His	Gly Pro Pro	Arg Pro Gly	Ala Leu Thr	Pro Thr Pro Ser										
	325		330		335									
Leu Ser Ser	Gln Ala Leu	Pro Ser Pro	Arg Leu Pro	Thr Thr Asp Gly										
	340		345		350									
Ala His Pro	Gln Pro Ile	Ser Pro Ile	Pro Gly Gly	Val Ser Ser Ser										
	355		360		365									
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Gln Ala Gly	Ser Leu Val													
	385		390											

<210> 39  
 <211> 1933  
 <212> DNA  
 <213> Homo sapiens

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<210> 40  
 <211> 374  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
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 20 25 30  
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 35 40 45  
 Pro Pro Tyr Val Ile Asn Leu Asp Pro Ala Val His Glu Val Pro Phe  
 50 55 60  
 Pro Ala Asn Ile Asp Ile Arg Asp Thr Val Lys Tyr Lys Glu Val Met  
 65 70 75 80



Lys Gln Tyr Gly Leu Gly Pro Asn Gly Gly Ile Val Thr Ser Leu Asn  
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 Leu Phe Ala Thr Arg Phe Asp Gln Val Met Lys Phe Ile Glu Lys Ala  
                             100                            105                            110  
 Gln Asn Met Ser Lys Tyr Val Leu Ile Asp Thr Pro Gly Gln Ile Glu  
                             115                            120                            125  
 Val Phe Thr Trp Ser Ala Ser Gly Thr Ile Ile Thr Glu Ala Leu Ala  
                             130                            135                            140  
 Ser Ser Phe Pro Thr Val Val Ile Tyr Val Met Asp Thr Ser Arg Ser  
                             145                            150                            155                            160  
 Thr Asn Pro Val Thr Phe Met Ser Asn Met Leu Tyr Ala Cys Ser Ile  
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 Leu Tyr Lys Thr Lys Leu Pro Phe Ile Val Val Met Asn Lys Thr Asp  
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 Ile Ile Asp His Ser Phe Ala Val Glu Trp Met Gln Asp Phe Glu Ala  
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 Phe Gln Asp Ala Leu Asn Gln Glu Thr Thr Tyr Val Ser Asn Leu Thr  
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 Arg Ser Met Ser Leu Val Leu Asp Glu Phe Tyr Ser Ser Leu Arg Val  
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 Val Gly Val Ser Ala Val Leu Gly Thr Gly Leu Asp Glu Leu Phe Val  
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 Gln Val Thr Ser Ala Ala Glu Glu Tyr Glu Arg Glu Tyr Arg Pro Glu  
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 Tyr Glu Arg Leu Lys Lys Ser Leu Ala Asn Ala Glu Ser Gln Gln Gln  
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 Arg Glu Gln Leu Glu Arg Leu Arg Lys Asp Met Gly Ser Val Ala Leu  
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 Asp Ala Gly Thr Ala Lys Asp Ser Leu Ser Pro Val Leu His Pro Ser  
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 Asp Leu Ile Leu Thr Arg Gly Thr Leu Asp Glu Glu Asp Glu Glu Ala  
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 Asp Ser Asp Thr Asp Asp Ile Asp His Arg Val Thr Glu Glu Ser His  
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 Glu Glu Pro Ala Phe Gln Asn Phe Met Gln Glu Ser Met Ala Gln Tyr  
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 Trp Lys Arg Asn Asn Lys  
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&lt;210&gt; 41

&lt;211&gt; 2795

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

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&lt;210&gt; 42

&lt;211&gt; 468

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

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Gly Ser Gly Glu Ala Arg Gly Cys Arg Ala Ala Ala Asp Gly Ser Leu	20	25	30
Gln Trp Glu Val Gly Gly Trp Arg Trp Trp Gly Leu Ser Arg Ala Phe	35	40	45
Thr Val Lys Pro Glu Gly Arg Asp Ala Gly Glu Val Gly Ala Ser Gly	50	55	60
Ala Pro Ser Pro Pro Leu Ser Gly Leu Gln Ala Val Phe Leu Pro Gln	65	70	75
Gly Phe Pro Asp Ser Val Ser Pro Asp Tyr Leu Pro Tyr Gln Leu Trp	85	90	95
Asp Ser Val Gln Ala Phe Ala Ser Ser Leu Ser Gly Ser Leu Ala Thr	100	105	110
Gln Ala Val Leu Leu Gly Ile Gly Val Gly Asn Ala Lys Ala Thr Val	115	120	125
Ser Ala Ala Thr Ala Thr Trp Leu Val Lys Asp Ser Thr Gly Met Leu	130	135	140
Gly Arg Ile Val Phe Ala Trp Trp Lys Gly Ser Lys Leu Asp Cys Asn	145	150	155
Ala Lys Gln Trp Arg Leu Phe Ala Asp Ile Leu Asn Asp Val Ala Met	165	170	175
Phe Leu Glu Ile Met Ala Pro Val Tyr Pro Ile Cys Phe Thr Met Thr	180	185	190
Val Ser Thr Ser Asn Leu Ala Lys Cys Ile Val Ser Val Ala Gly Gly	195	200	205
Ala Thr Arg Ala Ala Leu Thr Val His Gln Ala Arg Arg Asn Asn Met	210	215	220
Ala Asp Val Ser Ala Lys Asp Ser Ser Gln Glu Thr Leu Val Asn Leu	225	230	235
Ala Gly Leu Leu Val Ser Leu Leu Met Leu Pro Leu Val Ser Gly Cys	245	250	255
Pro Gly Phe Ser Leu Gly Cys Phe Phe Phe Leu Thr Ala Leu His Ile	260	265	270
Tyr Ala Asn Tyr Arg Ala Val Arg Ala Leu Val Met Glu Thr Leu Asn	275	280	285
Glu Gly Arg Leu Arg Leu Val Leu Lys His Tyr Leu Gln Arg Gly Glu	290	295	300
Val Leu Asp Pro Thr Ala Ala Asn Arg Met Glu Pro Leu Trp Thr Gly	305	310	315
Phe Trp Pro Ala Pro Ser Leu Ser Leu Gly Val Pro Leu His Arg Leu			

325 330 335  
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 370 375 380  
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 385 390 395 400  
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 Trp Val Val Val Lys Glu Thr His Glu Val Leu Asp Met Leu Phe Pro  
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 Lys Phe Leu Lys Gly Leu Gln Asp Ala Gly Trp Lys Thr Glu Lys His  
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 Gln Leu Glu Val Asp Glu Trp Arg Ala Thr Trp Leu Leu Ser Pro Glu  
 450 455 460  
 Lys Lys Val Leu  
 465

&lt;210&gt; 43

&lt;211&gt; 2980

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

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&lt;210&gt; 44

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

```

Met Leu Met Pro Leu Cys Gly Leu Leu Trp Trp Trp Trp Cys Cys Cys
  1             5             10            15

Ser Gly Trp Tyr Cys Tyr Gly Leu Cys Ala Pro Ala Pro Gln Met Leu
  20             25            30

Arg His Gln Gly Leu Leu Lys Cys Arg Cys Arg Met Leu Phe Asn Asp
  35             40            45

Leu Lys Val Phe Leu Leu Arg Arg Pro Pro Gln Ala Pro Leu Pro Met
  50             55            60

His Gly Asp Pro Gln Pro Pro Gly Leu Ala Ala Asn Asn Thr Leu Pro
  65             70            75            80

Ala Leu Gly Ala Gly Gly Trp Ala Gly Trp Arg Gly Pro Arg Glu Val
  85             90            95

Val Gly Arg Glu Pro Pro Pro Val Pro Pro Pro Pro Pro Leu Pro Pro
 100            105            110

Ser Ser Val Glu Asp Asp Trp Gly Gly Pro Ala Thr Glu Pro Pro Ala
 115            120            125

Ser Leu Leu Ser Ser Ala Ser Ser Asp Asp Phe Cys Lys Glu Lys Thr
 130            135            140

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Glu Asp Arg Tyr Ser Leu Gly Ser Ser Leu Asp Ser Gly Met Arg Thr  
 145 150 155 160  
 Pro Leu Cys Arg Ile Cys Phe Gln Gly Pro Glu Gln Gly Glu Leu Leu  
 165 170 175  
 Ser Pro Cys Arg Cys Asp Gly Ser Val Lys Cys Thr His Gln Pro Cys  
 180 185 190  
 Leu Ile Lys Trp Ile Ser Glu Arg Gly Cys Trp Ser Cys Glu Leu Cys  
 195 200 205  
 Tyr Tyr Lys Tyr His Val Ile Ala Ile Ser Thr Lys Asn Pro Leu Gln  
 210 215 220  
 Trp Gln Ala Ile Ser Leu Thr Val Ile Glu Lys Val Gln Val Ala Ala  
 225 230 235 240  
 Ala Ile Leu Gly Ser Leu Phe Leu Ile Ala Ser Ile Ser Trp Leu Ile  
 245 250 255  
 Trp Ser Thr Phe Ser Pro Ser Ala Arg Trp Gln Arg Gln Asp Leu Leu  
 260 265 270  
 Phe Gln Ile Cys Tyr Gly Met Tyr Gly Phe Met Asp Val Val Cys Ile  
 275 280 285  
 Gly Leu Ile Ile His Glu Gly Pro Ser Val Tyr Arg Ile Phe Lys Arg  
 290 295 300  
 Trp Gln Ala Val Asn Gln Gln Trp Lys Val Leu Asn Tyr Asp Lys Thr  
 305 310 315 320  
 Lys Asp Leu Glu Asp Gln Lys Ala Gly Gly Arg Thr Asn Pro Arg Thr  
 325 330 335  
 Ser Ser Ser Thr Gln Ala Asn Ile Pro Ser Ser Glu Glu Glu Thr Ala  
 340 345 350  
 Gly Thr Pro Ala Pro Glu Gln Gly Pro Ala Gln Ala Ala Gly His Pro  
 355 360 365  
 Ser Gly Pro Leu Ser His His His Cys Ala Tyr Thr Ile Leu His Ile  
 370 375 380  
 Leu Ser His Leu Arg Pro His Glu Gln Arg Ser Pro Pro Gly Ser Ser  
 385 390 395 400  
 Arg Glu Leu Val Met Arg Val Thr Thr Val  
 405 410

&lt;210&gt; 45

&lt;211&gt; 3666

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

aagacaagta ttccctgaaat gtgtcacctg gctctgttgg ccaagccagc agtgccacaa 60  
 gagaagcagc tgccatggcc cagtgcacacc tggagtgttt gacgatgctt tgtgtccatg 120

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tggccccctaa ccaggcccttt ctcacagcca catagcatcc ccaggccctgc tgcactgggc 180
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aaaaaa

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<210> 46  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
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 Leu Ser Ala Gly Pro Pro Gln Ser Gln Ser Leu Val Leu Gly Pro Lys  
 20 25 30  
 Ala Gly Pro Arg Gly Cys Arg Lys Gln Ser Val Ala Ser Lys Trp Gly  
 35 40 45  
 Leu Ser Tyr Pro Leu Gln Cys Val Gly Ala Glu Arg Ser Leu Gly Asp  
 50 55 60  
 Phe Ser Ala Gly Pro Pro Tyr Ser Arg Asp Pro Ser Val Phe Lys Thr  
 65 70 75 80  
 Lys Gln Glu Gly Lys Glu Glu Trp Arg Asn Ser Ser Val Leu Thr Leu  
 85 90 95  
 Phe Pro Leu Val Ser Ala Val Leu Gly Pro Leu Cys Thr Ser Tyr His  
 100 105 110  
 Phe Pro Leu Glu Ser Ala Pro Gln Gly Arg Val Arg Asp Glu Asp Ser  
 115 120 125  
 Gly Cys Lys Glu Val Ser Gln Leu Gly Asn Gly Ser Gly Gln Leu  
 130 135 140

<210> 47  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
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 tggccatgga cctgcggatg ttgtcccggg agctctccct ctacctggaa caccaagtc 180  
 ggggtggggt cctcggtcg ggggtgggct tatcccttat cctgggcttc agcgtcgctt 240  
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 cggtgcagta caggaatgaa cttattaaaa ctgcagatgg aggacagatt tcaactggact 480  
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 ggctactttt taattactat ttgacaacct gccttcagtc ttcagttaat aagcaccgac 960  
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 ttgataagcg attcacttca gtcattgttg gataccaaac aattgatgat tattatactg 1080  
 atgccagtc gagtcctaga ctgaagtcag taggaattcc agtatttgtt ctaaatctcg 1140



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tggatgatgt tttctcacc agtcattgcta ttccaataga aactgctaag caaaatccta 1200
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caagacagtc cacttacatg gatcgtgtct tcaagcaatt tgtgcaagcc atggttgagc 1320
atggacatga actctcttaa catgtagttc tttgggtgca ttttgtctga accacaattg 1380
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ctttgtagca acaaattaaa tatagtatta gattgttact tacgtagatt ttatttttac 1560
tatgccttac caagtacatc cttaaacaaa gtagtatgta catgaaattg cacttaacca 1620
aaactattgt gtaaaacaaa ttttaattcc tcagggtttt aatttaaact agtatttttt 1680
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ttaggactaa cttatgtttt ataattgatta taatttacat gcttattttt aaaatagtat 1980
atgtggacac atatatatca ttattattaaa ataaattcta ccatttttaa aaaaaaaaaa 2040
aaaaaaaaaa aa 2052

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&lt;210&gt; 48

&lt;211&gt; 409

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

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Met Gln Arg Leu Ala Met Asp Leu Arg Met Leu Ser Arg Glu Leu Ser
  1             5             10            15

Leu Tyr Leu Glu His Gln Val Arg Val Gly Phe Phe Gly Ser Gly Val
          20             25            30

Gly Leu Ser Leu Ile Leu Gly Phe Ser Val Ala Tyr Ala Phe Tyr Tyr
  35             40            45

Leu Ser Ser Ile Ala Lys Lys Pro Gln Leu Val Thr Gly Gly Glu Ser
  50             55            60

Phe Ser Arg Phe Leu Gln Asp His Cys Pro Val Val Thr Glu Thr Tyr
  65             70            75            80

Tyr Pro Thr Val Trp Cys Trp Glu Gly Arg Gly Gln Thr Leu Leu Arg
          85             90            95

Pro Phe Ile Thr Ser Lys Pro Pro Val Gln Tyr Arg Asn Glu Leu Ile
          100            105            110

Lys Thr Ala Asp Gly Gly Gln Ile Ser Leu Asp Trp Phe Asp Asn Asp
          115            120            125

Asn Ser Thr Cys Tyr Met Asp Ala Ser Thr Arg Pro Thr Ile Leu Leu
          130            135            140

Leu Pro Gly Leu Thr Gly Thr Ser Lys Glu Ser Tyr Ile Leu His Met
          145            150            155            160

Ile His Leu Ser Glu Glu Leu Gly Tyr Arg Cys Val Val Phe Asn Asn
          165            170            175

Arg Gly Val Ala Gly Glu Asn Leu Leu Thr Pro Arg Thr Tyr Cys Cys
          180            185            190

Ala Asn Thr Glu Asp Leu Glu Thr Val Ile His His Val His Ser Leu

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195                      200                      205  
 Tyr Pro Ser Ala Pro Phe Leu Ala Ala Gly Val Ser Met Gly Gly Met  
 210                      215                      220  
 Leu Leu Leu Asn Tyr Leu Gly Lys Ile Gly Ser Lys Thr Pro Leu Met  
 225                      230                      235                      240  
 Ala Ala Ala Thr Phe Ser Val Gly Trp Asn Thr Phe Ala Cys Ser Glu  
 245                      250                      255  
 Ser Leu Glu Lys Pro Leu Asn Trp Leu Leu Phe Asn Tyr Tyr Leu Thr  
 260                      265                      270  
 Thr Cys Leu Gln Ser Ser Val Asn Lys His Arg His Met Phe Val Lys  
 275                      280                      285  
 Gln Val Asp Met Asp His Val Met Lys Ala Lys Ser Ile Arg Glu Phe  
 290                      295                      300  
 Asp Lys Arg Phe Thr Ser Val Met Phe Gly Tyr Gln Thr Ile Asp Asp  
 305                      310                      315  
 Tyr Tyr Thr Asp Ala Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile  
 325                      330                      335  
 Pro Val Leu Cys Leu Asn Ser Val Asp Asp Val Phe Ser Pro Ser His  
 340                      345                      350  
 Ala Ile Pro Ile Glu Thr Ala Lys Gln Asn Pro Asn Val Ala Leu Val  
 355                      360                      365  
 Leu Thr Ser Tyr Gly Gly His Ile Gly Phe Leu Glu Gly Ile Trp Pro  
 370                      375                      380  
 Arg Gln Ser Thr Tyr Met Asp Arg Val Phe Lys Gln Phe Val Gln Ala  
 385                      390                      395                      400  
 Met Val Glu His Gly His Glu Leu Ser  
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&lt;210&gt; 49

&lt;211&gt; 2505

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

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 ggcggttggg ccggtgatac ccgggcgctt tatagtcccg ccgcctcttc ctccacctcc 120  
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 aatgcatact tccccttggtg acaagtgggg atgaggaaga agaaaaggat tataaaggcc 480  
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 aagaaaactgg tcagaaaata aataattcacg agtactacct tgggaatatg ttggccaaga 660  
 accttctatt tgaaaaagaa cgagaagcag aagaaaagga aaatcaaatt gagattccca 720

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acaagcagtg ttgtcatgta aaaaaaaaa aaaaaaaaa aaaaaa 2505

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&lt;210&gt; 50

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

```

Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
  1              5              10              15

Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg
      20              25              30

Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
      35              40              45

Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
      50              55              60

Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Cys Ile
      65              70              75              80

Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Lys Asp Tyr Lys
      85              90              95

Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe Lys Gln Ser Ser
      100              105              110

Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu Val Cys His Gly
      115              120              125

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Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr Gly Gln Lys Ile  
 130 135 140  
 Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala Lys Asn Leu Leu  
 145 150 155 160  
 Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys Ser Asn Glu Ile  
 165 170 175  
 Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly  
 180 185 190  
 Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser  
 195 200 205  
 Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu  
 210 215 220  
 Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr  
 225 230 235 240  
 Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val  
 245 250 255  
 Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu  
 260 265 270  
 Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe  
 275 280 285  
 Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe  
 290 295 300  
 Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr  
 305 310 315 320  
 Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys  
 325 330 335  
 Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp  
 340 345 350  
 Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp  
 355 360 365  
 Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu  
 370 375 380  
 Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu  
 385 390 395 400  
 Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly  
 405 410 415  
 Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val  
 420 425 430  
 Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr  
 435 440 445

Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro  
 450 455 460

Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser  
 465 470 475 480

Leu Pro Asn

<210> 51  
 <211> 2986  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
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<210> 52

<211> 640

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Cys Arg Ala Phe Pro Trp Glu Lys Glu Leu Lys Asp Lys His Pro
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```

```

Ser Leu Phe Gln Ala Leu Leu Glu Met Asp Leu Leu Thr Val Pro Arg
              20              25              30

```

```

Asn Gln Asn Glu Ser Val Ser Glu Ile Gly Gly Lys Ile Phe Glu Lys
      35              40              45

```

```

Ala Val Lys Arg Leu Ser Ser Ile Asp Gly Leu His Gln Ile Ser Ser
      50              55              60

```

```

Ile Val Pro Phe Leu Thr Asp Ser Ser Cys Cys Gly Tyr His Lys Ala
      65              70              75              80

```

```

Ser Tyr Tyr Leu Ala Val Phe Tyr Glu Thr Gly Leu Asn Val Pro Arg
              85              90              95

```

```

Asp Gln Leu Gln Gly Met Leu Tyr Ser Leu Val Gly Gly Gln Gly Ser
      100             105             110

```

```

Glu Arg Leu Ser Ser Met Asn Leu Gly Tyr Lys His Tyr Gln Gly Ile
      115             120             125

```

```

Asp Asn Tyr Pro Leu Asp Trp Glu Leu Ser Tyr Ala Tyr Tyr Ser Asn
      130             135             140

```

```

Ile Ala Thr Lys Thr Pro Leu Asp Gln His Thr Leu Gln Gly Asp Gln
      145             150             155             160

```

```

Ala Tyr Val Glu Thr Ile Arg Leu Lys Asp Asp Glu Ile Leu Lys Val
      165             170             175

```

```

Gln Thr Lys Glu Asp Gly Asp Val Phe Met Trp Leu Lys His Glu Ala
      180             185             190

```

```

Thr Arg Gly Asn Ala Ala Ala Gln Gln Arg Leu Ala Gln Met Leu Phe
      195             200             205

```

```

Trp Gly Gln Gln Gly Val Ala Lys Asn Pro Glu Ala Ala Ile Glu Trp
      210             215             220

```

```

Tyr Ala Lys Gly Ala Leu Glu Thr Glu Asp Pro Ala Leu Ile Tyr Asp
      225             230             235             240

```

```

Tyr Ala Ile Val Leu Phe Lys Gly Gln Gly Val Lys Lys Asn Arg Arg

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245										250					255				
Leu	Ala	Leu	Glu	Leu	Met	Lys	Lys	Ala	Ala	Ser	Lys	Gly	Leu	His	Gln				
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Ala	Val	Asn	Gly	Leu	Gly	Trp	Tyr	Tyr	His	Lys	Phe	Lys	Lys	Asn	Tyr				
		275					280						285						
Ala	Lys	Ala	Ala	Lys	Tyr	Trp	Leu	Lys	Ala	Glu	Glu	Met	Gly	Asn	Pro				
	290					295						300							
Asp	Ala	Ser	Tyr	Asn	Leu	Gly	Val	Leu	His	Leu	Asp	Gly	Ile	Phe	Pro				
305					310						315				320				
Gly	Val	Pro	Gly	Arg	Asn	Gln	Thr	Leu	Ala	Gly	Glu	Tyr	Phe	His	Lys				
				325						330				335					
Ala	Ala	Gln	Gly	Gly	His	Met	Glu	Gly	Thr	Leu	Trp	Cys	Ser	Leu	Tyr				
			340					345						350					
Tyr	Ile	Thr	Gly	Asn	Leu	Glu	Thr	Phe	Pro	Arg	Asp	Pro	Glu	Lys	Ala				
		355					360					365							
Val	Val	Trp	Ala	Lys	His	Val	Ala	Glu	Lys	Asn	Gly	Tyr	Leu	Gly	His				
	370					375					380								
Val	Ile	Arg	Lys	Gly	Leu	Asn	Ala	Tyr	Leu	Glu	Gly	Ser	Trp	His	Glu				
385					390						395				400				
Ala	Leu	Leu	Tyr	Tyr	Val	Leu	Ala	Ala	Glu	Thr	Gly	Ile	Glu	Val	Ser				
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Gln	Thr	Asn	Leu	Ala	His	Ile	Cys	Glu	Glu	Arg	Pro	Asp	Leu	Ala	Arg				
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Arg	Tyr	Leu	Gly	Val	Asn	Cys	Val	Trp	Arg	Tyr	Tyr	Asn	Phe	Ser	Val				
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Phe	Gln	Ile	Asp	Ala	Pro	Ser	Phe	Ala	Tyr	Leu	Lys	Met	Gly	Asp	Leu				
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Tyr	Tyr	Tyr	Gly	His	Gln	Asn	Gln	Ser	Gln	Asp	Leu	Glu	Leu	Ser	Val				
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Gln	Met	Tyr	Ala	Gln	Ala	Ala	Leu	Asp	Gly	Asp	Ser	Gln	Gly	Phe	Phe				
			485					490						495					
Asn	Leu	Ala	Leu	Leu	Ile	Glu	Glu	Gly	Thr	Ile	Ile	Pro	His	His	Ile				
		500						505					510						
Leu	Asp	Phe	Leu	Glu	Ile	Asp	Ser	Thr	Leu	His	Ser	Asn	Asn	Ile	Ser				
	515						520					525							
Ile	Leu	Gln	Glu	Leu	Tyr	Glu	Arg	Cys	Trp	Ser	His	Ser	Asn	Glu	Glu				
	530					535					540								
Ser	Phe	Ser	Pro	Cys	Ser	Leu	Ala	Trp	Leu	Tyr	Leu	His	Leu	Arg	Leu				
545					550					555				560					
Leu	Trp	Gly	Ala	Ile	Leu	His	Ser	Ala	Leu	Ile	Tyr	Phe	Leu	Gly	Thr				

565	570	575
Phe Leu Leu Ser Ile Leu Ile Ala Trp Thr Val Gln Tyr Phe Gln Ser		
580	585	590
Val Ser Ala Ser Asp Pro Pro Pro Arg Pro Ser Gln Ala Ser Pro Asp		
595	600	605
Thr Ala Thr Ser Thr Ala Ser Pro Ala Val Thr Pro Ala Ala Asp Ala		
610	615	620
Ser Asp Gln Asp Gln Pro Thr Val Thr Asn Asn Pro Glu Pro Arg Gly		
625	630	635
		640

<210> 53  
 <211> 1908  
 <212> DNA  
 <213> Homo sapiens

<400> 53

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ggcgacagag cgagactccg actcaaaaaa aaaaaaaaaa aaaaaaaaaa 1908

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<210> 54  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 54



Met Phe Leu Leu Ala Lys Ser Leu Gly Phe Cys Leu Ala Ile Gly Tyr  
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 Cys Leu Cys His Leu Pro Arg Val Gly Ala Leu Asp Ile Lys Gly Arg  
 20 25 30  
 Arg Arg Ser Val Leu Leu Leu Tyr Lys Ser Ser Met Gln Cys Ser Thr  
 35 40 45  
 Arg Val Leu Gln Ala Ile Pro Gly Lys Arg Ala Cys Trp Thr Met Val  
 50 55 60  
 Phe Asp Gly Thr Thr Gln Asp Ser Leu Val Thr Val Gln Phe Lys Gly  
 65 70 75 80  
 Asn Val Thr Tyr Arg Arg Val Val  
 85

&lt;210&gt; 55

&lt;211&gt; 2969

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2969

```

&lt;210&gt; 56

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

```

Met Ala Ala Ala Ala Gly Arg Ser Leu Leu Leu Leu Leu Ser Ser Arg
  1             5             10             15

```

```

Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly
      20             25             30

```

```

Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His
      35             40             45

```

```

Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val
      50             55             60

```

```

Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln
      65             70             75             80

```

```

Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg
      85             90             95

```

```

Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu
      100            105            110

```

```

Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr
      115            120            125

```

```

Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu
      130            135            140

```

```

Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val
      145            150            155            160

```

```

Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu
      165            170            175

```

```

Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile
      180            185            190

```

```

Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu
      195            200            205

```

Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile  
 210 215 220  
 Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu  
 225 230 235 240  
 Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp  
 245 250 255  
 Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr  
 260 265 270  
 Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu  
 275 280 285  
 Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His  
 290 295 300  
 Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu  
 305 310 315 320  
 Lys Asp Ala Ile Ala Gln Ala Glu Met Asp Leu Lys Arg Leu Arg Asp  
 325 330 335  
 Pro Leu Gln Val His Leu Pro Leu Arg Gln Ile Gly Glu Lys Asp  
 340 345 350

&lt;210&gt; 57

&lt;211&gt; 1727

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

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<210> 58  
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 <212> PRT  
 <213> Homo sapiens

<400> 58  
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 Pro Pro Leu Ala Val Val Leu Arg Gly Gln Pro Gly Pro Val Thr Leu  
 35 40 45  
 Leu Phe Lys Glu Cys Val Cys Arg Val Ala Gly Leu Leu Thr Val Leu  
 50 55 60  
 Cys Val Gly Trp Val Phe Ser Leu Phe Leu Leu Phe Glu Val Pro Ser  
 65 70 75 80  
 Phe Gln Ser Leu Thr Leu Ser Pro Leu Pro Leu Pro Ser Ser Val Glu  
 85 90 95  
 Cys Cys Cys Ala Arg Val Arg Ala Ala Leu His Thr Gly Pro Leu Gly  
 100 105 110  
 Cys Val Asn  
 115

<210> 59  
 <211> 2617  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
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 aactctcccg tgaggctgca cccgtgtggg tagcactgga agcggcactg ttgtcattgt 600  
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```

&lt;210&gt; 60

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

```

Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys
  1             5             10            15

```

```

Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln
  20             25            30

```

```

Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu
  35             40            45

```

```

Val Phe Lys Tyr Lys Thr Phe Cys Pro Val Arg Tyr Met Gln Pro His
  50             55            60

```

```

Arg Ser Ser Leu Cys Leu His Phe Thr Ser Tyr Val Phe Ile Leu Ser
  65             70            75            80

```

```

Thr Trp Gly Ser Leu Arg Thr Tyr Ser Thr Asp Leu Lys Lys Lys Lys
  85             90            95

```

```

Leu Pro Gly Ser Ile Ser Val Ser Glu
  100            105

```

&lt;210&gt; 61

&lt;211&gt; 1457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 61

```

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```

&lt;210&gt; 62

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

```

Met Ala Glu Gly Glu Lys Asn Gln Asp Phe Thr Phe Lys Met Glu Ser
  1              5              10              15

Pro Ser Asp Ser Ala Val Val Leu Pro Ser Thr Pro Gln Ala Ser Ala
  20              25              30

Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln Pro Met Ser
  35              40              45

Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser Phe Asn Ser
  50              55              60

Ser Tyr Asn Val Val Lys Arg Leu Lys Val Glu Ser Glu Glu Asn Asp
  65              70              75              80

Gln Thr Phe Ser Glu Lys Pro Ala Ser Ser Thr Glu Glu Asn Cys Leu
  85              90              95

Glu Phe Gln Glu Ser Phe Lys His Ile Asp Ser Glu Phe Glu Glu Asn
 100              105              110

Thr Asn Leu Lys Asn Thr Leu Lys Asn Leu Asn Val Cys Glu Ser Gln
 115              120              125

Ser Leu Asp Ser Gly Ser Cys Ser Ala Leu Gln Asn Glu Phe Val Ser
 130              135              140

```

Glu Lys Leu Pro Lys Gln Arg Leu Asn Ala Glu Lys Ala Lys Leu Val  
 145 150 155 160  
 Lys Gln Val Gln Glu Lys Glu Asp Leu Leu Arg Arg Leu Lys Leu Val  
 165 170 175  
 Lys Met Tyr Arg Ser Lys Asn Asp Leu Ser Gln Leu Gln Leu Leu Ile  
 180 185 190  
 Lys Lys Trp Arg Ser Cys Ser Gln Leu Leu Leu Tyr Glu Leu Gln Ser  
 195 200 205  
 Ala Val Ser Glu Glu Asn Lys Lys Leu Ser Leu Thr Gln Leu Ile Asp  
 210 215 220  
 His Tyr Gly Leu Asp Asp Lys Leu Leu His Tyr Asn Arg Ser Glu Glu  
 225 230 235 240  
 Glu Phe Ile Asp Val  
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<210> 63  
 <211> 4093  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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&lt;210&gt; 64

&lt;211&gt; 893

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

```

Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile
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```

Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu
      20                      25                      30

```

```

Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro
  35                      40                      45

```

```

Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu
  50                      55                      60

```

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Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro
  65                      70                      75                      80

```

```

Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu

```



85	90	95
Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys 100 105 110		
Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp 115 120 125		
Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp 130 135 140		
Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly 145 150 155 160		
Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile 165 170 175		
Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys 180 185 190		
Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu 195 200 205		
Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln 210 215 220		
Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr 225 230 235 240		
Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val 245 250 255		
Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile 260 265 270		
Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val Met Gln 275 280 285		
Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser 290 295 300		
Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro 305 310 315 320		
Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser 325 330 335		
Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His 340 345 350		
Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu 355 360 365		
Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile 370 375 380		
Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys 385 390 395 400		
Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe		

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Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu						
	435		440		445	
Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr						
	450		455		460	
Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met						
	465		470		475	480
Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly						
	485		490		495	
Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys						
	500		505		510	
Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys						
	515		520		525	
Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp						
	530		535		540	
Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe						
	545		550		555	560
Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile						
	565		570		575	
Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp						
	580		585		590	
Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala						
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Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn						
	610		615		620	
Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser						
	625		630		635	640
Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val						
	645		650		655	
Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys						
	660		665		670	
Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys						
	675		680		685	
Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr						
	690		695		700	
Ser Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val						
	705		710		715	720
Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser						

	725		730		735
Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr	740		745		750
Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser	755		760		765
Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile	770		775		780
Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val	785		790		795
Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu	805		810		815
Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val	820		825		830
Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser	835		840		845
Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp	850		855		860
His Tyr Leu Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys	865		870		875
Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu	885		890		

&lt;210&gt; 65

&lt;211&gt; 3033

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

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&lt;210&gt; 66

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

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Met Asn Met Ala Ala Phe Leu Ala Leu Val Val Ala Val Leu Arg Phe
  1             5             10            15

Ile Gln Leu Lys Pro Lys Val Leu Asn Pro Trp Leu Asn Ile Ser Gly
          20             25            30

Leu Val Ala Leu Cys Leu Ala Ser Phe Gly Met Thr Leu Leu Gly Asn
  35             40            45

Phe Gln Leu Thr Asn Asp Glu Ile His Asn Val Gly Thr Ser Leu
  50             55            60

Thr Phe Gly Phe Gly Thr Leu Thr Cys Trp Ile Gln Ala Ala Leu Thr
  65             70            75            80

Leu Lys Val Asn Ile Lys Asn Glu Gly Arg Arg Val Gly Ile Pro Arg
          85             90            95

Val Ile Leu Ser Ala Ser Ile Thr Leu Cys Val Val Leu Tyr Phe Ile
          100            105           110

Leu Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp Gly
          115            120           125

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Leu Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu Phe  
130 135 140

Arg His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn Phe  
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Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln Thr Asp  
165 170 175

Gln Val

<210> 67

<211> 504

<212> DNA

<213> Homo sapiens

<400> 67

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aaaaaaaaa aaaaaaaaaa aaaa 504

<210> 68

<211> 130

<212> PRT

<213> Homo sapiens

<400> 68

Met Gly Phe Lys Thr Phe Gln Gly Pro Leu Ser Met Pro Leu Val Pro  
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Trp Thr Leu Ser Leu Gly Cys Leu Leu Ser Pro Ser Val Leu Pro Gln  
20 25 30

Ser Thr Asp Phe Ser His Ser Ala Val Ser Ile Gln Pro Cys Pro Leu  
35 40 45

Asp Leu Asp Thr Trp Leu Pro Asn Pro Val Pro Gly Asn Pro Asp Ser  
50 55 60

Thr Arg His Phe Leu Leu Pro Pro Glu Ala Ile Trp Pro Glu Thr Thr  
65 70 75 80

Asn Ala Ala Ser His Pro Glu Ser Gly Thr Gly Thr Phe Arg Thr Pro  
85 90 95

Pro Ser Leu Thr Leu Cys Pro Arg Pro Val Ile Gln Trp Leu Ala Phe  
100 105 110

Ser Met Gly Lys Thr Arg Ala Pro Pro Thr Thr Thr Ala Ser Ser Leu  
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Ile Pro  
130

<210> 69  
<211> 3103  
<212> DNA  
<213> Homo sapiens

<400> 69  
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<210> 70

<211> 453

<212> PRT

<213> Homo sapiens

<400> 70

Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys  
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Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly  
 20 25 30

Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val  
 35 40 45

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln  
 50 55 60

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro  
 65 70 75 80

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly  
 85 90 95

Leu Ala Met Phe Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys  
 100 105 110

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe Trp Phe Phe  
 115 120 125

Lys Phe Ala Ala Ala Ile Ala Ile Ile Ile Gly Ala Phe Phe Ile Pro  
 130 135 140

Glu Gly Thr Phe Thr Thr Val Trp Phe Tyr Val Gly Met Ala Gly Ala  
 145 150 155 160

Phe Cys Phe Ile Leu Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His  
 165 170 175

Ser Trp Asn Glu Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg  
 180 185 190

Cys Trp Tyr Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu  
 195 200 205

Ser Leu Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala  
 210 215 220

Ser Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys  
 225 230 235 240

Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser Gln  
 245 250 255

Pro Arg Ser Gly Leu Leu Gln Ser Ser Val Ile Thr Val Tyr Thr Met  
 260 265 270

Tyr Leu Thr Trp Ser Ala Met Thr Asn Glu Pro Glu Thr Asn Cys Asn  
275 280 285

Pro Ser Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr Ser Thr Val Pro  
290 295 300

Lys Glu Gly Gln Ser Val Gln Trp Trp His Ala Gln Gly Ile Ile Gly  
305 310 315 320

Leu Ile Leu Phe Leu Leu Cys Val Phe Tyr Ser Ser Ile Arg Thr Ser  
325 330 335

Asn Asn Ser Gln Val Asn Lys Leu Thr Leu Thr Ser Asp Glu Ser Thr  
340 345 350

Leu Ile Glu Asp Gly Gly Ala Arg Ser Asp Gly Ser Leu Glu Asp Gly  
355 360 365

Asp Asp Val His Arg Ala Val Asp Asn Glu Arg Asp Gly Val Thr Tyr  
370 375 380

Ser Tyr Ser Phe Phe His Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile  
385 390 395 400

Met Met Thr Leu Thr Asn Trp Tyr Arg Tyr Glu Pro Ser Arg Glu Met  
405 410 415

Lys Ser Gln Trp Thr Ala Val Trp Val Lys Ile Ser Ser Ser Trp Ile  
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Gly Ile Val Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr  
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Asn Arg Asp Phe Asp  
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<210> 71

<211> 1981

<212> DNA

<213> Homo sapiens

<400> 71

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&lt;210&gt; 72

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
          20             25             30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
          35             40             45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
          50             55             60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
          65             70             75             80

Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
          85             90             95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
          100            105            110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
          115            120            125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
          130            135            140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
          145            150            155            160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
          165            170            175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
          180            185            190

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Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
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 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln  
 340 345 350  
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
 355 360 365  
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
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 420 425 430  
 Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
 435 440 445  
 Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
 450 455 460  
 Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu  
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 Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala  
 485 490

&lt;210&gt; 73

&lt;211&gt; 3098

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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&lt;210&gt; 74

&lt;211&gt; 132

&lt;212&gt; PRT

<213> Homo sapiens

<400> 74

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Leu Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser Leu Asn Trp
 20             25             30

Arg Glu Phe Ser Phe Val Gln Ser Ser Leu Gly Phe Val Ala Leu Val
 35             40             45

Leu Ser Thr Leu His Thr Leu Thr Tyr Gly Trp Thr Arg Ala Phe Glu
 50             55             60

Glu Ser Arg Tyr Lys Phe Tyr Leu Pro Pro Thr Phe Thr Leu Thr Leu
 65             70             75             80

Leu Val Pro Cys Val Val Ile Leu Ala Lys Ala Leu Phe Leu Leu Pro
 85             90             95

Cys Ile Ser Arg Arg Leu Ala Arg Ile Arg Arg Gly Trp Glu Arg Glu
100            105            110

Ser Thr Ile Lys Phe Thr Leu Pro Thr Asp His Ala Leu Ala Glu Lys
115            120            125

Thr Ser His Val
130

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<210> 75

<211> 922

<212> DNA

<213> Homo sapiens

<400> 75

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ggttatgggg agcctgaggt ttatgggcc tgtgtatccc cttctccggg cccagcctg 180
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<210> 76

<211> 106

<212> PRT

<213> Homo sapiens

<400> 76

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 1           5           10           15

Pro Ala Trp Pro Thr Gly Leu Pro Leu Val Pro Val Pro Leu Val Val
          20           25           30

Gly Asp Gly Ala Ala Ala Arg Gly Val Met Gly Leu Gly Ser Val Phe
          35           40           45

Tyr Arg Pro Pro Arg Gly Pro Gln Trp Leu Pro Gly Glu Pro Asp Gly
          50           55           60

Ala Pro Glu Gly Tyr Arg Leu Gly Gly Pro Ser Leu Arg Val Trp Gly
          65           70           75           80

Gln Ala Leu Ala Ser Ala Ala Ser Gln Ser Pro Ser His Leu Pro Leu
          85           90           95

Lys Ile Gln Ser Leu Leu Trp Met Ser Leu
          100           105

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<210> 77  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

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<400> 77
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tgcccctgcg tgcccgtggc gtggcctcag ggctctgcgt gctggccagc tggctcaccg 180
ccttcgtcct caccaagtc ttcctgccag tggtagacac cttcggcctc cagggtgcctt 240
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gccaacatgg tgaaaccccc tctctactaa aaaatacaaa aaagctgggt gtggtggcac 660
acaccgtag tccagctac ttgggaggct gaggcagcat tgcttgaacc cgggaggtgg 720
aggctgcaat gagctgagat catgccattg cactccagcc tgggcaacga gagtgaact 780
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<210> 78  
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 <212> PRT  
 <213> Homo sapiens

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<400> 78
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 1           5           10           15

Leu Leu Met Ser Glu Val Leu Pro Leu Arg Ala Arg Gly Val Ala Ser
          20           25           30

Gly Leu Cys Val Leu Ala Ser Trp Leu Thr Ala Phe Val Leu Thr Lys
          35           40           45

Ser Phe Leu Pro Val Val Ser Thr Phe Gly Leu Gln Val Pro Phe Phe
          50           55           60

```

Phe Phe Ala Ala Ile Cys Leu Val Ser Leu Val Phe Thr Gly Cys Cys  
 65 70 75 80

Val Pro Glu Thr Lys Gly Arg Ser Leu Glu Gln Ile Glu Ser Phe Phe  
 85 90 95

Arg Thr Gly Arg Arg Ser Phe Leu Arg  
 100 105

<210> 79  
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 <212> DNA  
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<400> 79  
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 agccagaaga gtgcatgagc tggaaaagggt gaaaagaaga tgcctagaga atggcaattt 300  
 aaaagaaaaa gatatacttg ttttgccctt tgacctgacc gacctgggtt cccatgaagc 360  
 ggctaccaaa gctgttctcc aggagtttgg tagaatcgac attctgggtca acaatggtgg 420  
 aatgtcccg cgttctctgt gcatggatac cagcttggtt gtctacagaa agctaataga 480  
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 cattggatac tgtgctagca agcatgctct ccgggggttt tttaatggcc ttcgaacaga 660  
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 gactttgctt ccaacatgga atgaaataaa aaataataaa taaaagattg ccatgaatct 1200  
 tgcaaaaaaa aaaaaaaaaa aaaa 1224

<210> 80  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
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Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu  
 20 25 30

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu  
 35 40 45

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu  
 50 55 60

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
 65 70 75 80

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu	Glu	
				85					90				95			
Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu	Asp	Leu	
				100					105				110			
Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	Leu	Gln	Glu	
				115					120				125			
Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	Met	Ser	Gln	Arg	
				130					135				140			
Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	Arg	Lys	Leu	Ile	Glu	
145				150				155				160				
Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	Lys	Cys	Val	Leu	Pro	His	
				165				170				175				
Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	Val	Thr	Val	Asn	Ser	Ile	Leu	
				180				185				190				
Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	
				195				200				205				
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210				215				220								
Pro	Gly	Ile	Ile	Val	Ser	Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	
225				230				235				240				
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Asn	Gly	Asp	Gln	Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	
				260				265				270				
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275				280				285								
Gln	Pro	Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	
290				295				300								
Ala	Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	
305				310				315				320				
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	Thr	
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Lys His Asp																

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<400> 83  
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<211> 19

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<400> 101

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19

<210> 102

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<213> Artificial Sequence

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<210> 103

<211> 21

<212> DNA

<213> Artificial Sequence

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21

<210> 104

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<210> 105

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<212> DNA

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<223> oligonucleotide

<400> 105

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21

<210> 106

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 106

attctgctct tcctcttct c

21

<210> 107

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 107

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<210> 110  
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<400> 114  
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<210> 115  
<211> 21  
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<400> 115  
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<210> 116  
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<210> 117  
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<400> 117  
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<210> 118  
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<400> 118  
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<210> 119  
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<210> 120  
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<400> 120  
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<210> 121  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 121  
Met Gly Leu Lys Asn Ser Arg Phe Trp Glu Pro Ser Met Leu Ser Leu  
1 5 10 15  
Ser Pro Leu Leu Ser Thr Ser Leu Pro Asn Glu Arg Val Thr Glu Asn  
20 25 30  
Cys Phe Phe Ile Asn Arg Ser Phe Leu Ile Val Ser Gly Phe Asp Thr  
35 40 45  
Ser Val Val  
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<400> 122  
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20 25 30  
Thr Leu Ala Leu Ser Leu Ala Leu Thr Tyr Arg Leu Gly Pro Gly Ser  
35 40 45  
Val Leu Leu Ala Pro Arg Ser Pro Trp Arg Leu Gln Lys Pro Pro Pro  
50 55 60  
Ala Gly Gly Leu Pro His Ser Gln Leu Pro Ala Arg Gln Trp Gly Leu  
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85 90 95  
Pro Pro Ser Ile Cys  
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             20                    25                    30  
 Arg Pro Leu Leu Leu Leu Leu Leu Pro Pro Glu Leu Arg  
             35                    40                    45  
 Leu Cys Phe Gly Leu Leu Val Ser Gly Gln Phe Leu Val Val Leu Leu  
             50                    55                    60  
 Arg Leu Arg Gly Pro Asp Leu Phe Leu His His Arg Ile Val His Leu  
     65                    70                    75                    80  
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             20                    25                    30  
 Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg Leu  
             35                    40                    45  
 Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val Asn  
             50                    55                    60  
 Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr Leu  
     65                    70                    75                    80  
 Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu Gln  
             85                    90                    95  
 Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser Pro  
             100                    105                    110  
 Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro Ser  
             115                    120                    125  
 Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser Leu  
             130                    135                    140



Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys Lys  
 145 150 155 160  
 Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu Val  
 165 170 175  
 Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly Thr  
 180 185 190  
 Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His Arg  
 195 200 205  
 Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp Ala  
 210 215 220  
 Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile Ser  
 225 230 235 240  
 Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg Pro  
 245 250 255  
 Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser Leu  
 260 265 270  
 Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly Ala  
 275 280 285  
 His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser Gly  
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 Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val  
 35 40 45  
 Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln  
 50 55 60  
 Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys  
 65 70 75 80  
 Glu Asp Gln Cys Cys Pro Thr Ser Met Gly Ser Gln Gln Ala Asn Leu  
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Glu Tyr Pro Trp Ser Thr Pro Cys Pro Pro Gly Thr Cys Pro Cys Gly  
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Trp Arg Val Ser Arg Arg Lys Thr Leu Ala Pro Thr Ala Ala Pro  
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<210> 126

<211> 91

<212> PRT

<213> Homo sapiens

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Ile Pro Ser His Gly Ala Ile Ile Phe His Cys Val Tyr Lys Thr Thr  
 35 40 45

Phe Cys Gln Ser Thr His Pro Trp Ile Thr Ser Ala Phe Leu Lys Gly  
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Ala Phe Thr Ser Gln Thr Gln Phe Ser Val Gly Glu Gly Val Arg Gly  
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<213> Homo sapiens

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Val Pro Pro Gly Ser Val Ala Ser Ser Met Ser Leu Gln Ala Gly Arg  
 35 40 45

Cys Gly Asn Pro Val Val Leu Pro Gln Pro Met Pro Pro Gly Leu Leu  
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Cys Met Asn Glu Cys Ser Leu Val Pro Gly Leu Gly Arg Gly Gln Val  
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Asn Ser Arg Val

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

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Met Pro Ala Trp Asp Asp Glu Ala His Ser Glu Gln Met Leu Phe Phe
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Phe Leu Arg Gln Ser Leu Ala Leu Thr Pro Arg Leu Glu Cys Ser Gly
          50             55             60

Ala Ile Ser Ala His Cys Lys Leu Cys Leu Pro Gly Ser Ser Asp Ser
          65             70             75             80

Pro Thr Ser Ala Ser Arg Val Ala Gly Ile Thr Pro Pro Cys Pro Ala
          85             90             95

Asn Phe Cys Val Phe Ser Arg Asp Gly Val Ser Pro Cys Trp Pro Gly
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Trp Ser Arg Thr Pro Asp Leu Arg
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&lt;210&gt; 129

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

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Pro Ser Asp Ser Ala Val Val Leu Pro Ser Thr Pro Gln Ala Ser Ala
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Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln Pro Met Ser
          35             40             45

Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser Phe Asn Ser
          50             55             60

Ser Tyr Asn Val Val Lys Arg Leu Lys Val Glu Ser Glu Glu Asn Asp
          65             70             75             80

Gln Thr Phe Ser Glu Lys Pro Ala Ser Ser Thr Glu Glu Asn Cys Leu
          85             90             95

Glu Phe Gln Glu Ser Phe Lys His Ile Asp Ser Glu Phe Glu Glu Asn
          100            105            110

Thr Asn Leu Lys Asn Thr Leu Thr Ala Ile Ser Met Ser Val Asn Leu
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Ser His Leu Ile Leu Asp His Ala Val Leu Ser Lys Met Ser Leu

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                   20                          25                          30  
  
 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp  
                   35                          40                          45  
  
 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser  
   50                          55                          60  
  
 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
   65                          70                          75                          80  
  
 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
                           85                          90                          95  
  
 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro  
                   100                          105                          110  
  
 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val  
                   115                          120                          125  
  
 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro  
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 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr  
  145                          150                          155                          160  
  
 Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro  
                   165                          170                          175  
  
 Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu  
                   180                          185                          190  
  
 Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp  
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 Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe  
   210                          215                          220  
  
 Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro  
  225                          230                          235                          240  
  
 Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser  
                   245                          250                          255  
  
 Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala  
                   260                          265                          270

Ser Lys Glu Val Ser Glu Lys Ala Lys Leu Tyr Ser  
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<210> 131

<211> 175

<212> PRT

<213> Homo sapiens

<400> 131

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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
65 70 75 80

Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Arg Ala Glu Met Arg  
130 135 140

Gly Thr Pro Gly His Arg Trp Gly Arg Ala Arg Arg Leu Glu Gly Asp  
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Ala Met Pro Pro Ala Arg Gln Arg Leu Pro Val Gln Val Pro Val  
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<210> 132

<211> 147

<212> PRT

<213> Homo sapiens

<400> 132

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Leu Leu Met Ser Glu Val Leu Pro Leu Arg Ala Arg Gly Val Ala Ser  
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Gly Leu Cys Val Leu Ala Ser Trp Leu Thr Ala Phe Val Leu Thr Lys  
35 40 45

Ser Phe Leu Pro Val Val Ser Thr Phe Gly Leu Gln Val Pro Phe Phe

50 55 60  
Phe Phe Ala Ala Ile Cys Leu Val Ser Leu Val Phe Thr Gly Cys Cys  
65 70 75 80  
Val Pro Glu Thr Lys Gly Arg Ser Leu Glu Gln Ile Glu Phe Leu Leu  
85 90 95  
Pro His Gly Glu Lys Val Leu Leu Ala Leu Gly Gln Gly Pro Arg Leu  
100 105 110  
Glu Gly Ala Lys Pro Pro Val Ala Gly Pro Leu Cys Trp Leu Cys Lys  
115 120 125  
Glu Asp Pro Ala Leu Pro Ser Gln Val Leu Trp Ala Pro Gln Gly Thr  
130 135 140  
Ser Trp Thr  
145

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/19351

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07H 21/04; C07K 14/705; C12N 15/09; 15/63; C12Q 1/68

US CL : 536/23.1, 24.3; 435/7.2. 69.1, 320.1; 530/350, 300

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 24.3; 435/7.2. 69.1, 320.1; 530/350, 300

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, JAPIO, BIOSIS, WPIDS, CAPLUS, EMBASE, N-GENESEQ35, N-ISSUED, EMBL-EST58, PIR60, SWISS-PROT37, SPTREMBL19, EMBL58

search terms: secreted proteins, 98862, 98846, VB11

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EMBASE EST-58 , Accession No. AA458581, NID g2183488, HILLIER et al., 'aa12e01.rl Soares-NhHMPu-S1 Homo sapiens cDNA clone IMAGE:813048 5' similar to contains element PTR5 repetitive element; mRNA sequence, 9 June, 1997	1-11
0		
X	Database EMBASE EST 158, Accession No. Z99943, NID g2887308, PEARCE, A., 'Human DNA sequence from PAC 313L4 on chromosome 1q24. Contains ESTs.' 12 February 1998	44-45



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*E* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

16 NOVEMBER 1999

Date of mailing of the international search report

11 JAN 2000

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

NIRMAL S. BASI

Telephone No. (703) 308-0196

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/19351

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:  
1-11 and 44-45
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.



# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/19351

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)1-11, drawn to polynucleotide comprising SEQ ID NO:1, fragments thereof, expression vector containing said sequence, cell transformed with said vector, polypeptide of SEQ ID NO:2, fragments of the polypeptide of SEQ ID NO:2 and process for preparing said polypeptide.

Group II, claim(s)12-13, drawn to polynucleotide comprising SEQ ID NO:3, fragments thereof, polypeptide of SEQ ID NO:4 and fragments of the polypeptide of said polypeptide.

Group III, claim(s)14-15, drawn to polynucleotide comprising SEQ ID NO:5, fragments thereof, polypeptide of SEQ ID NO:6 and fragments of the polypeptide of said polypeptide.

Group IV, claim(s)16-17, drawn to polynucleotide comprising SEQ ID NO:7, fragments thereof, polypeptide of SEQ ID NO:8 and fragments of the polypeptide of said polypeptide.

Group V, claim(s)18-19, drawn to polynucleotide comprising SEQ ID NO:9, fragments thereof, polypeptide of SEQ ID NO:10 and fragments of the polypeptide of said polypeptide.

Group VI, claim(s)20-21, drawn to polynucleotide comprising SEQ ID NO:11, fragments thereof, polypeptide of SEQ ID NO:12 and fragments of the polypeptide of said polypeptide.

Group VII, claim(s)22-23, drawn to polynucleotide comprising SEQ ID NO:13, fragments thereof, polypeptide of SEQ ID NO:14 and fragments of the polypeptide of said polypeptide.

Group VIII, claim(s)24-25, drawn to polynucleotide comprising SEQ ID NO:15, fragments thereof, polypeptide of SEQ ID NO:16 and fragments of the polypeptide of said polypeptide.

Group IX, claim(s)26-27, drawn to polynucleotide comprising SEQ ID NO:17, fragments thereof, polypeptide of SEQ ID NO:18 and fragments of the polypeptide of said polypeptide.

Group X, claim(s)28-29, drawn to polynucleotide comprising SEQ ID NO:19, fragments thereof, polypeptide of SEQ ID NO:20 and fragments of the polypeptide of said polypeptide.

Group XI, claim(s)30-31, drawn to polynucleotide comprising SEQ ID NO:21, fragments thereof, polypeptide of SEQ ID NO:22 and fragments of the polypeptide of said polypeptide.

Group XII, claim(s)32-33, drawn to polynucleotide comprising SEQ ID NO:23, fragments thereof, polypeptide of SEQ ID NO:24 and fragments of the polypeptide of said polypeptide.

Group XIII, claim(s)34-35, drawn to polynucleotide comprising SEQ ID NO:25, fragments thereof, polypeptide of SEQ ID NO:26 and fragments of the polypeptide of said polypeptide.

Group XIV, claim(s)36-37, drawn to polynucleotide comprising SEQ ID NO:27, fragments thereof, polypeptide of SEQ ID NO:28 and fragments of the polypeptide of said polypeptide.

Group XV, claim(s)38-39, drawn to polynucleotide comprising SEQ ID NO:29, fragments thereof, polypeptide of SEQ ID NO:30 and fragments of the polypeptide of said polypeptide.

Group XVI, claim(s)40-41, drawn to polynucleotide comprising SEQ ID NO:31, fragments thereof, polypeptide of SEQ ID NO:32 and fragments of the polypeptide of said polypeptide.

Group XVII, claim(s)42-43, drawn to polynucleotide comprising SEQ ID NO:33, fragments thereof, polypeptide of SEQ ID NO:34 and fragments of the polypeptide of said polypeptide.

Group XVIII, claim(s)44-45, drawn to polynucleotide comprising SEQ ID NO:35, fragments thereof, polypeptide of SEQ ID NO:36 and fragments of the polypeptide of said polypeptide.

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PCT/US99/19351

Group XIX, claim(s)46-47, drawn to polynucleotide comprising SEQ ID NO:37, fragments thereof, polypeptide of SEQ ID NO:38 and fragments of the polypeptide of said polypeptide.

Group XX, claim(s)48-49, drawn to polynucleotide comprising SEQ ID NO:39, fragments thereof, polypeptide of SEQ ID NO:40 and fragments of the polypeptide of said polypeptide.

Group XXI, claim(s)50-51, drawn to polynucleotide comprising SEQ ID NO:41, fragments thereof, polypeptide of SEQ ID NO:42 and fragments of the polypeptide of said polypeptide.

Group XXII, claim(s)52-53, drawn to polynucleotide comprising SEQ ID NO:43, fragments thereof, polypeptide of SEQ ID NO:44 and fragments of the polypeptide of said polypeptide.

Group XXIII, claim(s)54-55, drawn to polynucleotide comprising SEQ ID NO:45, fragments thereof, polypeptide of SEQ ID NO:46 and fragments of the polypeptide of said polypeptide.

Group XXIV, claim(s)56-57, drawn to polynucleotide comprising SEQ ID NO:47, fragments thereof, polypeptide of SEQ ID NO:48 and fragments of the polypeptide of said polypeptide.

Group XXV, claim(s)58-59, drawn to polynucleotide comprising SEQ ID NO:49, fragments thereof, polypeptide of SEQ ID NO:50 and fragments of the polypeptide of said polypeptide.

Group XXVI, claim(s)60-61, drawn to polynucleotide comprising SEQ ID NO:51, fragments thereof, polypeptide of SEQ ID NO:52 and fragments of the polypeptide of said polypeptide.

Group XXVII, claim(s)62-63, drawn to polynucleotide comprising SEQ ID NO:53, fragments thereof, polypeptide of SEQ ID NO:54 and fragments of the polypeptide of said polypeptide.

Group XXVIII, claim(s)64-65, drawn to polynucleotide comprising SEQ ID NO:55, fragments thereof, polypeptide of SEQ ID NO:56 and fragments of the polypeptide of said polypeptide.

Group XXIX, claim(s)66-67, drawn to polynucleotide comprising SEQ ID NO:57, fragments thereof, polypeptide of SEQ ID NO:58 and fragments of the polypeptide of said polypeptide.

Group XXX, claim(s)68-69, drawn to polynucleotide comprising SEQ ID NO:59, fragments thereof, polypeptide of SEQ ID NO:60 and fragments of the polypeptide of said polypeptide.

Group XXXI, claim(s)70-71, drawn to polynucleotide comprising SEQ ID NO:61, fragments thereof, polypeptide of SEQ ID NO:62 and fragments of the polypeptide of said polypeptide.

Group XXXII, claim(s)72-73, drawn to polynucleotide comprising SEQ ID NO:63, fragments thereof, polypeptide of SEQ ID NO:64 and fragments of the polypeptide of said polypeptide.

Group XXXIII, claim(s)74-75, drawn to polynucleotide comprising SEQ ID NO:65, fragments thereof, polypeptide of SEQ ID NO:66 and fragments of the polypeptide of said polypeptide.

Group XXXIV, claim(s)76-77, drawn to polynucleotide comprising SEQ ID NO:67, fragments thereof, polypeptide of SEQ ID NO:68 and fragments of the polypeptide of said polypeptide.

Group XXXV, claim(s)78-79, drawn to polynucleotide comprising SEQ ID NO:69, fragments thereof, polypeptide of SEQ ID NO:70 and fragments of the polypeptide of said polypeptide.

Group XXXVI, claim(s)80-81, drawn to polynucleotide comprising SEQ ID NO:71, fragments thereof, polypeptide of SEQ ID NO:72 and fragments of the polypeptide of said polypeptide.

Group XXXVII, claim(s)82-83, drawn to polynucleotide comprising SEQ ID NO:73, fragments thereof, polypeptide of SEQ ID NO:74 and fragments of the polypeptide of said polypeptide.

Group XXXVIII, claim(s)84-85, drawn to polynucleotide comprising SEQ ID NO:75, fragments thereof, polypeptide of SEQ ID NO:76 and fragments of the polypeptide of said polypeptide.

Group XXXIX, claim(s)86-87, drawn to polynucleotide comprising SEQ ID NO:77, fragments thereof, polypeptide of

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SEQ ID NO:78 and fragments of the polypeptide of said polypeptide.

Group XL, claim(s)88-89, drawn to polynucleotide comprising SEQ ID NO:79, fragments thereof, polypeptide of SEQ ID NO:80 and fragments of the polypeptide of said polypeptide.

The inventions listed as Groups I-XL do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The main invention is Group I, which is first product, first method of making the product and first method of using the product. Pursuant to 37 CFR 1.474 (d), these claims are considered by the ISA/US to constitute the main invention. The products of Groups II-XL do not share the same or corresponding special technical feature with group I because they are drawn to products having materially different structures and functions, each defines a separate invention over the art. Therefore, the claims are not linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C07H 21/04, C07K 14/705, C12N 15/09, 15/63, C12Q 1/68</b>		<b>A1</b>	(11) International Publication Number: <b>WO 00/11015</b>
			(43) International Publication Date: <b>2 March 2000 (02.03.00)</b>
(21) International Application Number: <b>PCT/US99/19351</b>		(74) Agent: <b>SPRUNGER, Suzanne, A.; American Home Products Corporation, Patent &amp; Trademark Dept. - 2B, One Campus Drive, Parsippany, NJ 07054 (US).</b>	
(22) International Filing Date: <b>24 August 1999 (24.08.99)</b>			
(30) Priority Data:		(81) Designated States: <b>AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</b>	
60/097,638      24 August 1998 (24.08.98)      US 60/097,659      24 August 1998 (24.08.98)      US 60/099,618      9 September 1998 (09.09.98)      US 60/102,092      28 September 1998 (28.09.98)      US 60/109,978      25 November 1998 (25.11.98)      US 60/113,645      23 December 1998 (23.12.98)      US 60/113,646      23 December 1998 (23.12.98)      US 09/379,246      23 August 1999 (23.08.99)      US			
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(54) Title: <b>SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM</b>			
(57) Abstract  Novel polynucleotides and the proteins encoded thereby are disclosed.			

FASTA search protocols. vc50\_1 demonstrated at least some similarity with sequences identified as AA193122 (zr39d05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665769 5', mRNA sequence), T26031 (Human gene signature HUMGS08267; standard; cDNA to mRNA), Z31718 (H.sapiens gene for myelin protein zero), and Z99943 (Human DNA sequence from PAC 313L4 on chromosome 1q24). The predicted amino acid sequence disclosed herein for vc50\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc50\_1 protein demonstrated at least some similarity to the sequence identified as K03242 (rat P0 myelin prepeptide), L24893 (myelin protein zero [Homo sapiens]), and M62860 (mouse peripheral myelin protein). Based upon sequence similarity, vc50\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vc50\_1 protein sequence centered around amino acid 181 of SEQ ID NO:36.

vc50\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "vc51\_1"

A polynucleotide of the present invention has been identified as clone "vc51\_1". vc51\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc51\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc51\_1 protein").

The nucleotide sequence of vc51\_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc51\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 12 to 24 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc51\_1 protein. If the "G" residue at position 388 of SEQ ID NO:37 were deleted, two alternative potential vc51\_1 reading frames and predicted amino acid sequences that could be

encoded by basepairs 333 to 1310 of SEQ ID NO:37 and by basepairs 139 to 522 of SEQ ID NO:37 are reported in SEQ ID NO:124 and SEQ ID NO:125, respectively.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc51\_1 should be approximately 1992 bp.

5       The nucleotide sequence disclosed herein for vc51\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc51\_1 demonstrated at least some similarity with sequences identified as T21514 (Human gene signature HUMGS02887; standard; cDNA to mRNA) and W52782 (zd13h06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340571  
10   5', mRNA sequence). The predicted amino acid sequence disclosed herein for vc51\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc51\_1 protein demonstrated at least some similarity to sequences identified as U90716 (human cell surface protein HCAR), Y07593 (coxsackie and adenovirus receptor protein [Homo sapiens]), Y10320 (mouse coxsackie  
15   and adenovirus receptor homolog), and W14146 (Human A33 antigen). Based upon sequence similarity, vc51\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the vc51\_1 protein sequence centered around amino acids 17, 216, 260, and 373 of SEQ ID NO:38, respectively.

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#### Clone "vc52\_1"

A polynucleotide of the present invention has been identified as clone "vc52\_1". vc52\_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the  
25   amino acid sequence of the encoded protein. vc52\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc52\_1 protein").

The nucleotide sequence of vc52\_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc52\_1 protein corresponding  
30   to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 19 to 31 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

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ggtttccctg aaggaagctg ctcacactga gatgagcctc tcagggcagg acctcttccc 3420
aagccctgca caccaccccc tgcagccctt ttggctcccc ttttccctgt gcctcagcac 3480
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&lt;210&gt; 36

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

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Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp Ser
  1           5           10          15

Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu Leu Thr
      20           25           30

Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu Ile Phe Val
      35           40           45

Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe Lys Ser Thr Ser
      50           55           60

Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser Phe Gln Pro Glu Gly
      65           70           75           80

Ala Asp Thr Thr Val Ser Phe Phe His Tyr Ser Gln Gly Gln Val Tyr
      85           90           95

Leu Gly Asn Tyr Pro Pro Phe Lys Asp Arg Ile Ser Trp Ala Gly Asp
      100          105          110

Leu Asp Lys Lys Asp Ala Ser Ile Asn Ile Glu Asn Met Gln Phe Ile
      115          120          125

His Asn Gly Thr Tyr Ile Cys Asp Val Lys Asn Pro Pro Asp Ile Val
      130          135          140

Val Gln Pro Gly His Ile Arg Leu Tyr Val Val Glu Lys Glu Asn Leu
      145          150          155          160

Pro Val Phe Pro Val Trp Val Val Val Gly Ile Val Thr Ala Val Val
      165          170          175

Leu Gly Leu Thr Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg
      180          185          190

Arg Lys Asn Ser Lys Arg Asp Tyr Thr Gly Ala Gln Ser Tyr Met His
      195          200          205

Ser

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&lt;210&gt; 37

&lt;211&gt; 1954

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

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gagacttggg ctggagccgc cctgggtgtc agcgggctcg gctcccgcgc acgctccggc 60
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa

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1954

&lt;210&gt; 38

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
  1             5             10             15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
          20             25             30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
          35             40             45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
          50             55             60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
          65             70             75             80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

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